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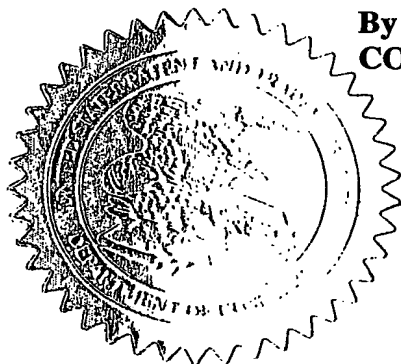
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**U.S. PATENT AND TRADEMARK OFFICE  
PROVISIONAL APPLICATION FOR PATENT COVER SHEET**

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT  
under 37 C.F.R. §1.53(b)(2)

Atty. Docket: KOPCHICK6

INVENTOR(S)/APPLICANT(S)			
LAST NAME	FIRST NAME	MI	RESIDENCE (CITY AND EITHER STATE OR FOREIGN COUNTRY)
KOPCHICK	John	J	Athens, OH
KELDER	Bruce		Athens, OH
BOYCE	Keith		Athens, OH
KRIETE	Andres		Athens, OH

☐ Additional inventors are being named on separately numbered sheets attached hereto

**TITLE OF THE INVENTION (280 characters max)**

DIAGNOSIS OF HYPERINSULINEMIA AND TYPE II DIABETES AND PROTECTION AGAINST SAME (II)

**CORRESPONDENCE ADDRESS**

Direct all correspondence to the address associated with Customer Number 001444, which is presently:

BROWDY AND NEIMARK, P.L.L.C.  
624 Ninth Street, N.W., Suite 300  
Washington, D.C. 20001-5303

**ENCLOSED APPLICATION PARTS (check all that apply)**

☒ Specification      Number of Pages    278      ☒ Applicant claims small entity status. See 37 C.F.R. §1.27

☐ Drawing(s)      Number of Sheets      ☐ Other (specify) \_\_\_\_\_

**METHOD OF PAYMENT (check one)**

☒ Credit Card Payment Form PTO-2038 is enclosed to cover the Provisional filing fee of

☐ \$160 large entity      ☒ \$80 small entity

☒ The Commissioner is hereby authorized to charge filing fees and credit Deposit Account Number 02-4035

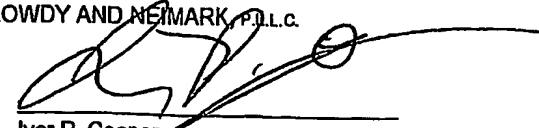
The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☐ No ☐ Yes, the name of the U.S. Government agency and the Government contract number are:

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.

Date: April 7, 2003

By:   
Iver P. Cooper  
Registration No.: 28,005

**DIAGNOSIS OF HYPERINSULINEMIA AND TYPE II DIABETES AND  
PROTECTION AGAINST SAME (II)**

*Cross-Reference to Related Applications*

5 In U.S. Provisional Appl. Ser. No. 60/\_\_\_\_\_ (our  
docket Kelder1-USA), filed March 31, 2003, we describe the  
identification of genes differentially expressed in normal  
vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic,  
or normal vs. type II diabetic mouse liver. Forward- and  
10 reverse-subtracted cDNA libraries were prepared, clones  
were isolated, and differentially expressed cDNA inserts  
were sequenced and compared with sequences in publicly  
available sequence databases. The corresponding mouse and  
human genes and proteins were identified.

15 Favorable genes/proteins so identified included (1) NP\_000767:  
cytochrome P450, subfamily IIIA (naphthepine oxidase), polypeptide 3;  
(2) AAG31034: SYT/SSX4 fusion protein ; and (3) NP\_003158:  
sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone  
(DHEA)-preferring, member 1; sulfotransferase family 2A,  
20 dehydroepiandrosterone (DHEA)-preferring, member 1. Unfavorable  
proteins included (4) NP\_004884: H2A histone family, member Y  
isoform 2; histone macroH2A1.2; histone macroH2A1.1; (5) AAH37738:  
Unknown (protein for MGC:33851); (6) NP\_068839: integral membrane  
protein 2B ; (7) CAA28659: S-protein ; and (8) AAA51560:  
25 alpha-1-antichymotrypsin precursor. Mixed proteins included (9)  
NP\_000769: cytochrome P450, subfamily IVA, polypeptide 11; fatty acid  
omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid  
omega-hydroxylase; (10) NP\_006206:serine (or cysteine) proteinase  
inhibitor, clade A ; (11) NP\_004489: one cut domain, family member 1;  
30 hepatocyte nuclear factor 6, alpha; and (12) NP\_775491:  
liver-specific uridine phosphorylase.

Gene chip technology was not used. Two of the genes  
(NM\_007818 and NM\_007822) were also identified in the  
present case.

35 The use of differential hybridization to identify genes and  
proteins is also described in our Ser. No. PCT/US00/12145 (Kopchick 3A-  
PCT), Ser. No. PCT/US00/12366 (Kopchick4A-PCT), and Ser. No. 60/400,052  
(Kopchick5).

**BACKGROUND OF THE INVENTION**Field of the Invention

The invention relates to various nucleic acid molecules and proteins, and their use in (1) diagnosing  
5 hyperinsulinemia and type II diabetes, or conditions associated with their development, and (2) protecting mammals (including humans) against them.

Description of the Background Art10 *Diabetes*

Diabetes mellitus is a pleiotropic disease of great complexity. The two major types have been termed type I or insulin-dependent diabetes mellitus (IDDM) and type II or non-insulin-dependent diabetes mellitus (NIDDM). Type II  
15 diabetes is the predominant form found in the Western world; fewer than 8% of diabetic Americans have the type I disease.

Type I diabetics are often characterized by their low or absent levels of circulating endogenous insulin, i.e., hypoinsulinemia (1). Islet cell antibodies causing damage  
20 to the pancreas are frequently present at diagnosis. Injection of exogenous insulin is required to prevent ketosis and sustain life.

Early Type II diabetics are often characterized by hyperinsulinemia and resistance to insulin. Late Type II  
25 diabetics may be normoinsulinemic or hypoinsulinemic. Type II diabetics are usually not insulin dependent or prone to ketosis under normal circumstances.

*Type II Diabetes*

30 Type II diabetes (formerly known as non-insulin dependent diabetes, NIDDM) is the most common form of elevated blood glucose (hyperglycemia). Type II diabetes is a metabolic disorder that affects approximately 17 million Americans. It is estimated that another 10 million  
35 individuals are "prone" to becoming diabetic. These vulnerable individuals can become resistant to insulin, a pancreatic hormone that signals glucose (blood sugar) uptake by fat and muscle. In order to maintain normal glucose



levels, the islet cells of the pancreas produce more insulin, resulting in a condition called hyperinsulinemia. When the pancreas can no longer produce enough insulin to compensate for the insulin resistance, and thereby maintain normal glucose levels, Type II diabetes (hyperglycemia) results.

Complications of diabetes (end organ damage) include retinopathy, neuropathy, and nephropathy (traditionally designated as microvascular complications) as well as atherosclerosis (a macrovascular complication).

Early stages of hyperglycemia can usually be controlled by an alteration in diet and increasing the amount of exercise, but drug treatment, including insulin, may be required. It has been shown that meticulous blood glucose control can often slow down or halt the progression of diabetic complications if caught early enough (1). However, tight metabolic control is extremely difficult to achieve.

Little is known about the disease progression from the normoinsulinemic state to the hyperinsulinemic state, and from the hyperinsulinemic state to the Type II diabetic state.

As stated above, type II diabetes is a metabolic disorder that is characterized by insulin resistance and impaired glucose-stimulated insulin secretion (2,3,4). However, Type II diabetes and atherosclerotic disease are viewed as consequences of having the insulin resistance syndrome (IRS) for many years (5). The current theory of the pathogenesis of Type II diabetes is often referred to as the "insulin resistance/islet cell exhaustion" theory. According to this theory, a condition causing insulin resistance compels the pancreatic islet cells to hypersecrete insulin in order to maintain glucose homeostasis. However, after many years of hypersecretion, the islet cells eventually fail and the symptoms of clinical diabetes are manifested. Therefore, this theory implies that, at some point, peripheral hyperinsulinemia will be an antecedent of Type II diabetes. Peripheral hyperinsulinemia

can be viewed as the difference between what is produced by the  $\beta$  cell minus that which is taken up by the liver. Therefore, peripheral hyperinsulinemia can be caused by increased  $\beta$  cell production, decreased hepatic uptake or  
5 some combination of both. It is also important to note that it is not possible to determine the origin of insulin resistance once it is established since the onset of peripheral hyperinsulinemia leads to a condition of global insulin resistance.

10

Multiple environmental and genetic factors are involved in the development of insulin resistance, hyperinsulinemia and type II diabetes. An important risk factor for the development of insulin resistance, hyperinsulinemia and type  
15 II diabetes is obesity, particularly visceral obesity (6,7,8). Type II diabetes exists world-wide, but in developed societies, the prevalence has risen as the average age of the population increases and the average individual becomes more obese.

20

Obesity is a serious and growing problem in the United States. Obesity-related health risks include high blood pressure, hardening of the arteries, cardiovascular disease, and Type II diabetes (also known as non-insulin-dependent diabetes mellitus, Type II diabetes) (9,10,11). Recent  
25 studies show that 85% of the individuals with Type II diabetes are obese (12).

#### *Growth Hormone*

30

Growth hormone has many roles, ranging from regulation of protein, fat and carbohydrate metabolism to growth  
35 promotion. GH is produced in the somatrophic cells of the anterior pituitary and exerts its effects either through the GH-induced action of IGF-I, in the case of growth promotion, or by direct interaction with the GHR on target cells including liver, muscle, adipose, and kidney cells. Hyposecretion of GH during development leads to dwarfism, and hypersecretion before puberty leads to gigantism. In adults, hypersecretion of GH results in acromegaly, a

clinical condition characterized by enlarged facial bones, hands, feet, fatigue and an increase in weight. Of those individuals with acromegaly, 25% develop type II diabetes. This may be due to insulin resistance caused by the high circulating levels of GH leading to high circulating levels of insulin (Kopchick et al., Annual Rev. Nutrition 1999. 19:437-61).

A further mode of GH action may be through the transcriptional regulation of a number of genes contributing to the physiological effects of GH.

#### *Transgenic Mice*

McGrane, et al., J. Biol. Chem. 263:11443-51 (1988) and Chen, et al., J. Biol. Chem., 269:15892-7 (1994) describe the genetic engineering of mice to express bovine growth hormone (bGH) or human growth hormone (hGH), respectively. These mice exhibited an enhanced growth phenotype. They also developed kidney lesions similar to those seen in diabetic glomerulosclerosis, see Yang, et al., Lab. Invest., 68:62-70 (1993). Ogueta, et al., J. Endocrinol., 165: 321-8 (2000) reported that transgenic mice expressing bovine GH develop arthritic disorder and self-antibodies.

Growth hormone genes and the proteins encoded by them can be converted into growth hormone antagonists by mutation, see Kopchick USP 5,350,836. Transgenic mice have been made that express the GH antagonists bGH-G119R or hGH G120R, and which exhibit a dwarf phenotype. Chen, et al., J. Biol. Chem., 263:15892-7 (1994); Chen, et al., Mol. Endocrinol, 5:1845-52 (1991); Chen, et al., Proc. Nat. Acad. Sci. USA 87:5061-5 (1990). These mice did not develop kidney lesions. See Yang (1993), supra.

Chen, et al., Endocrinol, 136:660-7 (1995) compared the effect of streptozotocin treatment in normal nontransgenic mice, and in mice transgenic for (1) a GH receptor antagonist, the G119R mutant of bovine growth hormone or (2) the E117L-mutant of bGH. (According to Chen's ref. 24, these large GH transgenic streptozotocin-treated mice

constitute an animal model for diabetes.)

Glomerulosclerosis was seen in diabetic (STZ-treated) nontransgenic mice and in diabetic bGH-E117L mice, but not in diabetic bGH-G119R (GH antagonist) mice.

5 Two of the proteins which mediate growth hormone activity are the growth hormone receptor and the growth hormone binding protein, encoded by the same gene in mice (GHR/BP). It is possible to genetically engineer mice so that the gene encoding these proteins is disrupted ("knocked-out"; inactivated), see Zhou, et al., Proc. Nat. Acad. Sci. (USA), 94:13215-20 (1997). Zhou, et al. inactivated the GHR/BP gene by replacing the 3' portion of exon 4 (which encodes a portion of the GH binding domains) and the 5' region of intron 4 with a neomycin gene cassette. 10 The modified gene was introduced into the target mice by homologous recombination. Like mice expressing a GH antagonist, homozygous GHR/BP-KO mice exhibit a dwarf phenotype. GHR/BP-KO mice, made diabetic by streptozotocin treatment, are protected from the development of diabetes-associated nephropathy. Bellush, et al., Endocrinol., 141:163-8 (2000). 15 20

#### *Differential/Subtractive Hybridization*

25 Zhang, et al., Kidney International, 56:549-558 (1999) identified genes up-regulated in 5/6 nephrectomized (subtotal renal ablation) mouse kidney by a PCR-based subtraction method. Ten known and nine novel genes were identified. The ultimate goal was to identify genes 30 involved in glomerular hyperfiltration and hypertrophy.

Melia, et al., Endocrinol., 139:688-95 (1998) applied subtractive hybridization methods for the identification of androgen-regulated genes in mouse kidney. The treatment mice were dosed with dihydrotestosterone, an androgen. 35 Kidney androgen-regulated protein gene was used as a positive control, as it is known to be up-regulated by DHT.

See also Holland, et al., Abstract 607, "Identification of Genes Possibly Involved in Nephropathy of Bovine Growth

Hormone Transgenic Mice" (Endocrine Society Meeting, June 22, 2000) and Coschigano, et al., Abstract 333, "Identification of Genes Potentially Involved in Kidney Protection During Diabetes" (Endocrine Society Meeting, June 22, 2000).

The following differential hybridization articles may also be of interest:

Wada, et al., "Gene expression profile in streptozotocin-induced diabetic mice kidneys undergoing glomerulosclerosis", *Kidney Int*, 59:1363-73 (2001);

Song, et al., "Cloning of a novel gene in the human kidney homologous to rat munc13S: its potential role in diabetic nephropathy", *Kidney Int.*, 53:1689-95 (1998);

Page, et al., "Isolation of diabetes-associated kidney genes using differential display", *Biochem. Biophys. Res. Comm.*, 232:49-53 (1997).

Peradi, "Subtractive hybridization claims: An efficient technique to detect overexpressed mRNAs in diabetic nephropathy," *Kidney Int.* 53:926-31 (1998).

Condorelli, *EMBO J.*, 17:3858-66 (1998).

See also WO00/66784 (differential hybridization screening for brown adipose tissue); PCT/US00/12366, filed May 5, 2000 (differential hybridization screening for liver).

*Identification of genes involved in hyperinsulinemia and type II diabetes*

High-fat diets have been shown to induce both obesity and Type II diabetes in laboratory animals (13). Surwit and colleagues demonstrated that male C57BL/6J mice are extremely sensitive to the diabetogenic effects of a high-fat diet when initiated at weaning. At six months of age, high-fat fed animals had significantly elevated fasting blood-glucose and insulin levels and also demonstrated a decrease in insulin sensitivity (14). Ahren and colleagues (15) reported evidence of insulin resistance as well as diminished glucose-stimulated insulin release, after feeding with a high-fat diet for 12 weeks. These mice also showed

elevated levels of total cholesterol, triglycerides, and free fatty acids, another hallmark of Type II diabetes.

Our attention recently has focused on the generation of liver mRNA expression profiles and the identification of genes involved in the genesis of the obesity-induced hyperinsulinemia and type-II diabetes. To date, no one has attempted to study the actual progression from the normal condition to that of hyperinsulinemia or from hyperinsulinemia to Type II diabetes in an attempt to identify genes that are up-regulated or down-regulated as the disease progresses.

In previous studies aimed at identifying genes involved in diabetes-induced glomerulosclerosis, differential display and traditional subtractive hybridization techniques were used (16-20). While effective for the identification of a few genes (e.g. hmunc13, PED/PEA-15, lactate dehydrogenase, amiloride sensitive sodium channel, ubiquitin-like protein, mdr 1, and  $\alpha$ -amyloid protein precursor as well as a few novel genes), these techniques can be quite labor intensive. The PCR-based method of subtractive hybridization requires less starting material, and allows the simultaneous isolation of all differentially expressed cDNAs into two groups (up-regulated and down-regulated).

However, the PCR-based method of subtractive hybridization is also quite labor-intensive, produced large numbers of false positive candidates and ultimately resulted in the identification of a relatively limited number of differentially expressed genes. (see Kelder1-USA application).

In order to expand the number of genes that can be analyzed simultaneously, several groups have begun to utilize DNA microarray analysis to measure differences in gene expression between normal and diseased states. However, these experiments have been limited in regards to the number of experimental conditions analyzed. DNA microarray analysis has been performed on normal, obese and diabetic mice (21). Also, the obesity and diabetes in the mouse models examined were caused by a specific endogenous

genetic mutation (22). The differentially expressed genes in the above models may be very different from genes differentially expressed due to diet-induced obesity and Type-II diabetes.

**SUMMARY OF THE INVENTION**

Differential hybridization techniques have been used to identify mouse genes that are differentially expressed in mice, depending upon their development of hyperinsulinemia or type II diabetes.

In essence, complementary RNA derived from normal mice, or mouse models of hyperinsulinemia or type II diabetes, was screened for hybridization with oligonucleotide probes each specific to a particular mouse gene, each gene in turn representative of a particular mouse gene cluster (Unigene). Mouse genes which were differentially expressed (normal vs. hyperinsulinemic, hyperinsulinemic vs. diabetic, or normal vs. diabetic), as measured by different levels of hybridization of the respective cRNA samples with the particular probe corresponding to that mouse gene) were identified. Related human genes and proteins were identified by sequence comparisons to the mouse gene or protein.

After identifying related human genes and proteins, one may formulate agents useful in screening humans at risk for progression toward hyperinsulinemia or toward type II diabetes.

Since the progression is from normal to hyperinsulinemic, and thence from hyperinsulinemic to type II diabetic, one may define mammalian subjects as being more favored or less favored, with normal subjects being more favored than hyperinsulinemic subjects, and hyperinsulinemic subjects being more favored than type II diabetic subjects. The subjects' state may then be correlated with their gene expression activity.

Thus, "favorable" human genes/proteins are defined as those corresponding to mouse genes which were less strongly expressed in mouse hyperinsulinemic liver than in control liver, or less strongly expressed in mouse type II diabetic liver than in hyperinsulinemic liver. (The control liver is the liver of a mouse which is normal vis-a-vis fasting insulin and fasting glucose levels. The term "normal", as



used herein, means normal relative to those parameters, and does not necessitate that the mouse be normal 'in every respect.) Likewise, one may define "unfavorable" human genes/proteins as those corresponding to mouse genes which were more strongly expressed in mouse hyperinsulinemic liver than in control liver, or more strongly expressed in mouse type II diabetic liver than in hyperinsulinemic liver.

As used herein, the term "corresponding" does not mean identical, but rather implies the existence of a statistically significant sequence similarity, such as one sufficient to qualify the human protein or gene as a homologous protein or DNA as defined below. The greater the degree of relationship as thus defined (i.e., by the statistical significance of each alignment used to connect the mouse cDNA to the human protein or gene, measured by an E value), the more close the correspondence. The connection may be direct (mouse gene to human protein) or indirect (e.g., mouse gene to human gene, human gene to human protein). By "mouse gene", we mean the mouse gene from which the gene chip DNA in question was derived.

In general, the human genes/proteins which most closely correspond, directly or indirectly, to the mouse genes are preferred, such as the one(s) with the highest, top two highest, top three highest, top four highest, top five highest, and top ten highest E values for the final alignment in the connection process. The human genes/proteins deemed to correspond to our mouse cDNA clones are identified in the Master Tables.

A human gene/protein corresponding to a mouse cDNA which was more strongly expressed in hyperinsulinemic liver than in either normal or type II diabetic liver (i.e.,  $C < HI$ ,  $HI > D$ ) will be deemed both "unfavorable", by virtue of the control:hyperinsulinemic comparison, and "favorable", by virtue of the hyperinsulinemic:diabetic comparison. This is one of several possible "mixed" expression patterns.

Thus, we can subdivide the "favorables" into wholly and partially favorables. Likewise, we can subdivide the unfavorables into wholly and partially unfavorables. The

genes/proteins with "mixed" expression patterns are, by definition, both partially favorable and partially unfavorable. In general, use of the wholly favorable or wholly unfavorable genes/proteins is preferred to use of the partially favorable or partially unfavorable ones.

Agents which bind the "favorable" and "unfavorable" nucleic acids (e.g., the agent is a substantially complementary nucleic acid hybridization probe), or the corresponding proteins (e.g., an antibody vs. the protein) may be used to evaluate whether a human subject is at increased or decreased risk for progression toward type II diabetes. A subject with one or more elevated "unfavorable" and/or one or more depressed "favorable" genes/proteins is at increased risk, and one with one or more elevated "favorable" and/or one or more depressed "unfavorable" genes/proteins is at decreased risk. One may further take into account whether the subject is normoinsulinemic or hyperinsulinemic at the time of the assay. If the subject is non-diabetic and normoinsulinemic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in hyperinsulinemic vs. normal livers. If the subject is already hyperinsulinemic, yet non-diabetic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in type II diabetic vs. hyperinsulinemic livers.

The assay may be used as a preliminary screening assay to select subjects for further analysis, or as a formal diagnostic assay.

The identification of the related genes and proteins may also be useful in protecting humans against these disorders.

Thus, Applicants contemplate:

(1) use of the "favorable" mouse DNAs of the Master Tables (below) to isolate or identify related human DNAs;

(2) use of human DNAs, related to favorable mouse DNAs, to express the corresponding human proteins;

5 (3) use of the corresponding human proteins (and mouse proteins, if biologically active in humans), to protect against the disorder(s);

10 (4) use of the corresponding mouse or human proteins, or nucleic acid probes derived from the mouse or human genes, in diagnostic agents, in assays to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage; and

15 (5) use of the corresponding human or mouse genes therapeutically in gene therapy, to protect against the disorder(s).

Moreover Applicants contemplate:

(1) use of the "unfavorable" mouse DNAs of the Master Tables to isolate or identify related human DNAs;

20 (2) use of the complement to the "unfavorable" mouse DNAs or related human DNAs, as antisense molecules to inhibit expression of the related human DNAs;

(3) use of the mouse or human DNAs to express the corresponding mouse or human proteins;

25 (4) use of the corresponding mouse or human proteins, in diagnostic agents, to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage;

30 (5) use of the corresponding mouse or human proteins in assays to determine whether a substance binds to (and hence may neutralize) the protein; and

(6) use of the neutralizing substance to protect against the disorder(s).

35 The related human DNAs may be identified by comparing the mouse sequence (or its AA translation product) to known human DNAs (and their AA translation products). If this is unsuccessful, human cDNA or genomic DNA libraries may be

14

screened using the mouse DNA as a probe.

## DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS OF THE INVENTION

### Subjects

5 A mouse is considered to be a diabetic subject if, regardless of its fasting plasma insulin level, it has a fasting plasma glucose level of at least 190 mg/dL. A mouse is considered to be a hyperinsulinemic subject if its  
10 fasting plasma insulin level is at least 0.67 ng/mL and it does not qualify as a diabetic subject. A mouse is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very limited manner.

15 A mouse is considered "obese" if its weight is at least 15% in excess of the mean weight for mice of its age and sex. A mouse which does not satisfy this standard may be characterized as "non-obese", the term "normal" being reserved for use in reference to glucose and insulin levels as previously described.

20 A human is considered a diabetic subject if, regardless of his or her fasting plasma insulin level, the fasting plasma glucose level is at least 126 mg/dL. A human is considered a hyperinsulinemic subject if the fasting plasma  
25 insulin level is more than 26 micro International Units/mL (it is believed that this is equivalent to 1.08 ng/mL), and does not qualify as a diabetic subject. A human is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very  
30 limited manner.

A human is considered "obese" if the body mass index (BMI) (weight divided by height squared) is at least 30 kg/m<sup>2</sup>. A human who does not satisfy this standard may be  
35 characterized as "non-obese", the term "normal" being reserved for use in reference to glucose and insulin levels as previously described.

A human is considered overweight if the BMI is at least 25 kg/m<sup>2</sup>. Thus, we define overweight to include obese

individuals, consistent with the recommendations of the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK). A human who does not satisfy this standard may be characterized as "non-overweight."

5

According to the Report of the Expert Committee on the Diagnosis and Classification of Diabetes Mellitus, Diabetes Care 20: 1183-97 (1997), the following are risk factors for diabetes type II:

10

older (e.g., at least 45; see below)

excessive weight (see below)

15

first-degree relative with diabetes mellitus

member of high risk ethnic group (black, Hispanic, Native American, Asian)

20

history of gestational diabetes mellitus or delivering a baby weighing more than 9 pounds (4.032 kg)

hypertensive (>140/90 mm Hg)

25

HDL cholesterol level >35 mg/dL (0.90 mmol/L)

triglyceride level >=250 mg/dL (2.83 mmol/L)

30

Hence, in a preferred embodiment, the diagnostic and protective methods of the present invention are applied to human subjects exhibiting one or more of the aforementioned risk factors. Likewise, in a preferred embodiment, they are applied to human subjects who, while not diabetic, exhibit impaired glucose homeostasis (110 to <126 mg/dL).

35

The risk of diabetes increases with age. Hence, in successive preferred embodiments, the age of the subjects is at least 45, at least 50, at least 55, at least 60, at least

65, at least 70, and at least 75.

With regard to excessive weight, NIDDK says that "The relative risk of diabetes increases by approximately 25 percent for each additional unit of BMI over 22." Hence, in  
5 successive preferred embodiments, the BMIs of the human subjects is at least 23, at least 24, at least 25 (i.e., overweight by our criterion), at least 26, at least 27, at least 28, at least 29, at least 30 (i.e., obese), at least 31, at least 32, at least 33, at least 34, at least 35, at  
10 least 36, at least 37, at least 38, at least 39, at least 40, or over 40.

#### **Genes/Proteins of Interest**

15 Favorable genes/proteins are those corresponding to genes less strongly expressed in hyperinsulinemic liver than in normal liver, or in type II diabetic liver as compared to hyperinsulinemic liver. Unfavorable genes/proteins are those corresponding to genes more strongly expressed in  
20 hyperinsulinemic liver than in normal liver, or in type II diabetic liver as compared to hyperinsulinemic liver.

Mixed genes/proteins are those exhibiting a combination of favorable and unfavorable behavior. A mixed gene/protein can be used as would a favorable gene/protein if its  
25 favorable behavior outweighs the unfavorable. It can be used as would an unfavorable gene/protein if its unfavorable behavior outweighs the favorable. Preferably, they are used in conjunction with other agents that affect their balance of favorable and unfavorable behavior. Use of mixed  
30 genes/proteins is, in general, less desirable than use of purely favorable or purely unfavorable genes/proteins.

For each of the differentially expressed genes, corresponding mouse and human proteins have been identified,  
35 as set forth in the Master Tables.

#### **Direct and Indirect Utility of Identified Nucleic Acid**

### Sequences and Related Molecules

The mouse or human genes (or fragments thereof) may be used directly. For diagnostic or screening purposes, they (or specific binding fragments thereof) may be labeled and used as hybridization probes. For therapeutic purposes, they (or specific binding fragments thereof) may be used as antisense reagents to inhibit the expression of the corresponding gene, or of a sufficiently homologous gene of another species.

Since each of the probes is representative of a full-length mouse gene, that is, it encodes an entire, functional protein, then it may be used in the expression of that protein. Likewise, if the corresponding human gene is known in full-length, it may be used to express the human protein. Such expression may be in cell culture, with the protein subsequently isolated and administered exogenously to subjects who would benefit therefrom, or in vivo, i.e., administration by gene therapy. Naturally, any DNA encoding the same protein, or a fragment or a mutant protein which retains the desired activity, may be used for the same purpose. The encoded protein of course has utility therapeutically and, in labeled or immobilized form, diagnostically.

The genes may also be used indirectly, that is, to identify other useful DNAs, proteins, or other molecules.

There thus are several ways that a human protein homologue of interest can be identified by database searching, including:

- 1) a DNA->DNA (BlastN) search for database DNAs closely related to the mouse gene identifies a known human gene, and the sequence of the human protein is deduced by the Genetic Code;
- 2) a DNA->Protein (BlastX) search for database proteins closely related to the translated DNA of the mouse gene identifies a known human protein; and



3) the sequence of the mouse protein is known or is deduced by the Genetic Code, and a Protein->Protein (BlastP) search for closely related database proteins identifies a known human protein.

5

Once a known human gene is identified, it may be used in further BlastN or BlastX searches to identify other human genes or proteins. Once a known human protein is identified, it may be used in further BlastP searches to identify other human proteins.

10

Searches may also take cognizance, intermediately, of known genes and proteins other than mouse or human ones, e.g., use the mouse sequence to identify a known rat sequence and then the rat sequence to identify a human one.

15

Thus, if we have identified a mouse gene, and it encodes a mouse protein which appears similar to a human protein, then that human protein may be used (especially in humans) for purposes analogous to the proposed use of the mouse protein in mice. Moreover, a specific binding fragment of an appropriate strand of the corresponding human gene or cDNA could be labeled and used as a hybridization probe (especially against samples of human mRNA or cDNA).

20

25

In determining whether the disclosed genes have significant similarities to known DNAs (and their translated AA sequences to known proteins), one would generally use the disclosed gene as a query sequence in a search of a sequence database. The results of several such searches are set forth in the Examples. Such results are dependent, to some degree, on the search parameters. Preferred parameters are set forth in Example 1. The results are also dependent on the content of the database. While the raw similarity score of a particular target (database) sequence will not vary with content (as long as it remains in the database), its informational value (in bits), expected value, and relative ranking can change. Generally speaking, the changes are small.

30

35

It will be appreciated that the nucleic acid and protein databases keep growing. Hence a later search may identify high scoring target sequences, which were not:  
5 uncovered by an earlier search because the target sequences were not previously part of a database.

Hence, in a preferred embodiment, the cognate DNAs and proteins include not only those set forth in the examples, but those which would have been highly ranked (top ten, more  
10 preferably top three, even more preferably top two, most preferably the top one) in a search run with the same parameters on the date of filing of this application.

If the known human DNA is appears to be a partial DNA,  
15 it may be used as a hybridization probe to isolate the full-length DNA. If the partial DNA encodes a biologically functional fragment of the cognate protein, it may be used in a manner similar to the full length DNA, i.e., to produce the functional fragment.

20 If we have indicated that an antagonist of a protein or other molecule is useful, then such an antagonist may be obtained by preparing a combinatorial library, as described below, of potential antagonists, and screening the library  
25 members for binding to the protein or other molecule in question. The binding members may then be further screened for the ability to antagonize the biological activity of the target. The antagonists may be used therapeutically, or, in suitably labeled or immobilized form, diagnostically.

30 If the identified DNA is related to a known protein, then substances known to interact with that protein (e.g., agonists, antagonists, substrates, receptors, second messengers, regulators, and so forth), and binding molecules which bind them, are also of utility. Such binding  
35 molecules can likewise be identified by screening a combinatorial library.

**Isolation of Full Length cDNAs Using Partial cDNAs as probes**

If it is determined that a DNA of the present invention is a partial DNA, and the cognate full length DNA is not listed in a sequence database, the available DNA may be used as a hybridization probe to isolate the full-length cDNA from a suitable cDNA library.

Stringent hybridization conditions are appropriate, that is, conditions in which the hybridization temperature is 5-10 deg. C. below the  $T_m$  of the cDNA as a perfect duplex.

#### Identification and Isolation of Homologous Genes/cDNAs Using a cDNA Probe

It may be that the sequence databases available do not include the sequence of any homologous gene, or at least of the homologous gene for a species of interest. However, given the cDNAs set forth above, one may readily obtain the homologous gene.

The possession of one DNA (the "starting DNA") greatly facilitates the isolation of homologous genes/cDNAs. If only a partial DNA is known, this partial DNA may first be used as a probe to isolate the corresponding full length DNA for the same species, and that the latter may be used as the starting DNA in the search for homologous genes.

The starting DNA, or a fragment thereof, is used as a hybridization probe to screen a cDNA or genomic DNA library for clones containing inserts which encode either the entire homologous protein, or a recognizable fragment thereof. The minimum length of the hybridization probe is dictated by the need for specificity. If the size of the library in bases is  $L$ , and the GC content is 50%, then the probe should have a length of at least  $l$ , where  $L = 4^l$ . This will yield, on average, a single perfect match in random DNA of  $L$  bases. The human cDNA library is about  $10^8$  bases and the human genomic DNA library is about  $10^{10}$  bases.

The library is preferably derived from an organism which is known, on biochemical evidence, to produce a homologous protein, and more preferably from the genomic DNA or mRNA of cells of that organism which are likely to be

relatively high producers of that protein. A cDNA library (which is derived from an mRNA library) is especially preferred.

If the organism in question is known to have substantially different codon preferences from that of the organism whose relevant cDNA or genomic DNA is known, a synthetic hybridization probe may be used which encodes the same amino acid sequence but whose codon utilization is more similar to that of the DNA of the target organism.

Alternatively, the synthetic probe may employ inosine as a substitute for those bases which are most likely to be divergent, or the probe may be a mixed probe which mixes the codons for the source DNA with the preferred codons (encoding the same amino acid) for the target organism.

By routine methods, the  $T_m$  of a perfect duplex of starting DNA is determined. One may then select a hybridization temperature which is sufficiently lower than the perfect duplex  $T_m$  to allow hybridization of the starting DNA (or other probe) to a target DNA which is divergent from the starting DNA. A 1% sequence divergence typically lowers the  $T_m$  of a duplex by 1-2°C, and the DNAs encoding homologous proteins of different species typically have sequence identities of around 50-80%. Preferably, the library is screened under conditions where the temperature is at least 20°C., more preferably at least 50°C., below the perfect duplex  $T_m$ . Since salt reduces the  $T_m$ , one ordinarily would carry out the search for DNAs encoding highly homologous proteins under relatively low salt hybridization conditions, e.g., <1M NaCl. The higher the salt concentration, and/or the lower the temperature, the greater the sequence divergence which is tolerated.

For the use of probes to identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries;

hybridization at 40°C in 50% formamide and 5xSSC); Murata et al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC). The conditions set forth in these articles may each be considered suitable for the purpose of isolating homologous genes.

## 10 Homologous Proteins and DNAs

A human protein can be said to be identifiable as homologous to a mouse gene (and hence to "correspond" to such gene) if

15

(1) its sequence can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and the expected value (E) of the alignment (the probability that such an alignment would have occurred by chance alone) is less than  $e^{-10}$ ,

20

(2) its sequence can be aligned to a human gene, using BlastX with the default parameters set forth below, and the cDNA of said human gene can be aligned to the mouse gene, using BlastN with the default parameters set forth below, and the E value for both alignments is less than  $e^{-10}$ ,

25

(3) its sequence can be aligned to a mouse protein, using BlastP with the default parameters set forth below, and that mouse protein can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and in both alignments the E value of the alignment is less than  $e^{-10}$ .

30

Naturally, if the human protein is encoded by the human gene of (2), or the mouse protein is encoded by the mouse gene of (3), the BlastX alignment will be satisfied.

35

Desirably, two or all three of these conditions (1)-(3) are

satisfied.

Preferably, for any of the alignments noted above, and more preferably for all of them, the E value is less than e-15, more preferably less than e-20, still more preferably less than e-40, even more preferably less than e-60, considerably more preferably less than e-80, and most preferably less than e-100. More preferably, for those conditions in which the mouse cDNA clone is indirectly connected to the human protein by virtue of two or more successive alignments, the E value is so limited for all of said alignments in the connecting chain.

BlastN and BlastX report very low expected values as "0.0". This does not truly mean that the expected value is exactly zero (since any alignment could occur by chance), but merely that it is so infinitesimal that it is not reported. The documentation does not state the cutoff value, alignments with explicit E values as low as e-178 (624 bits) have been reported as such, while a score of 636 bits was reported as "0.0".

Functionally homologous human proteins are also of interest. A human protein may be said to be functionally homologous to the mouse gene if (1) it can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and the E value of the alignment is less than e-50, and (2) the human protein has at least one biological activity in common with the mouse protein.

The human proteins of interest also include those that are substantially and/or conservatively identical (as defined below) to the homologous and/or functionally homologous human proteins defined above.

### Relevance of Favorable and Unfavorable Genes

If a gene is down-regulated in more favored mammals, or up-regulated in less favored mammals, (i.e., an "unfavorable gene") then several utilities are apparent.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject. Elevated levels are indicative of progression, or propensity to progression, to a less favored state, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product (or equivalent cDNA), the protein product, or a binding molecule specific for that product (e.g., an antibody which binds the product), or a downstream product which mediates the activity (e.g., a signaling intermediate) or a binding molecule (e.g., an antibody) therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said nucleic acid product, protein product, or downstream product (e.g., a signaling intermediate). Again, elevated levels are indicative of a present or future problem.

Thirdly, an agent which down-regulates expression of the gene may be used to reduce levels of the corresponding protein and thereby inhibit further damage. This agent could inhibit transcription of the gene in the subject, or translation of the corresponding messenger RNA. Possible inhibitors of transcription and translation include antisense molecules and repressor molecules. The agent could also inhibit a post-translational modification (e.g., glycosylation, phosphorylation, cleavage, GPI attachment) required for activity, or post-translationally modify the protein so as to inactivate it. Or it could be an agent which down- or up-regulated a positive or negative regulatory gene, respectively.

Fourthly, an agent which is an antagonist of the

messenger RNA product or protein product of the gene, or of a downstream product through which its activity is manifested (e.g., a signaling intermediate), may be used to inhibit its activity.

5        This antagonist could be an antibody, a peptide, a peptoid, a nucleic acid, a peptide nucleic acid (PNA) oligomer, a small organic molecule of a kind for which a combinatorial library exists (e.g., a benzodiazepine), etc. An antagonist is simply a binding molecule which, by  
10       binding, reduces or abolishes the undesired activity of its target. The antagonist, if not an oligomeric molecule, is preferably less than 500 daltons.

      Fifthly, an agent which degrades, or abets the degradation of, that messenger RNA, its protein product or a  
15       downstream product which mediates its activity (e.g., a signaling intermediate), may be used to curb the effective period of activity of the protein.

      If a gene is up-regulated in more favored mammals, or down-regulated in less favored animals then the utilities  
20       are converse to those stated above.

      First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject.  
25       Depressed levels are indicative of damage, or possibly of a propensity to damage, and clinicians may take appropriate preventative, curative or ameliorative action.

      Secondly, the messenger RNA product, the equivalent cDNA, protein product, or a binding molecule specific for  
30       those products, or a downstream product, or a signaling intermediate, or a binding molecule therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said protein product or downstream product. Again, depressed levels are indicative of a  
35       present or future problem.

      Thirdly, an agent which up-regulates expression of the gene may be used to increase levels of the corresponding protein and thereby inhibit further progression to a less



5 favored state. By way of example, it could be a vector which carries a copy of the gene, but which expresses the gene at higher levels than does the endogenous expression system. Or it could be an agent which up- or down-regulates a positive or negative regulatory gene.

10 Fourthly, an agent which is an agonist of the protein product of the gene, or of a downstream product through which its activity (of inhibition of progression to a less favored state) is manifested, or of a signaling intermediate may be used to foster its activity.

15 Fifthly, an agent which inhibits the degradation of that protein product or of a downstream product or of a signaling intermediate may be used to increase the effective period of activity of the protein.

#### **Mutant Proteins**

20 The present invention also contemplates mutant proteins (peptides) which are substantially identical (as defined below) to the parental protein (peptide). In general, the fewer the mutations, the more likely the mutant protein is to retain the activity of the parental protein. The effect of mutations is usually (but not always) additive. Certain individual mutations are more likely to be tolerated than  
25 others.

A protein is more likely to tolerate a mutation which

- (a) is a substitution rather than an insertion or deletion;
- (b) is an insertion or deletion at the terminus, rather than internally, or, if internal, is at a domain boundary, or a loop or turn, rather than in an alpha helix or beta strand;
- (c) affects a surface residue rather than an interior residue;
- (d) affects a part of the molecule distal to the binding site;
- (e) is a substitution of one amino acid for another of similar size, charge, and/or

hydrophobicity, and does not destroy a disulfide bond or other crosslink; and

(f) is at a site which is subject to substantial variation among a family of homologous proteins to which the protein of interest belongs.

These considerations can be used to design functional mutants.

#### *Surface vs. Interior Residues*

Charged residues almost always lie on the surface of the protein. For uncharged residues, there is less certainty, but in general, hydrophilic residues are partitioned to the surface and hydrophobic residues to the interior. Of course, for a membrane protein, the membrane-spanning segments are likely to be rich in hydrophobic residues.

Surface residues may be identified experimentally by various labeling techniques, or by 3-D structure mapping techniques like X-ray diffraction and NMR. A 3-D model of a homologous protein can be helpful.

#### *Binding Site Residues*

Residues forming the binding site may be identified by (1) comparing the effects of labeling the surface residues before and after complexing the protein to its target, (2) labeling the binding site directly with affinity ligands, (3) fragmenting the protein and testing the fragments for binding activity, and (4) systematic mutagenesis (e.g., alanine-scanning mutagenesis) to determine which mutants destroy binding. If the binding site of a homologous protein is known, the binding site may be postulated by analogy.

Protein libraries may be constructed and screened that a large family (e.g.,  $10^8$ ) of related mutants may be evaluated simultaneously.

Hence, the mutations are preferably conservative modifications as defined below.

### "Substantially Identical"

A mutant protein (peptide) is substantially identical to a reference protein (peptide) if (a) it has at least 10% of a specific binding activity or a non-nutritional biological activity of the reference protein, and (b) is at least 50% identical in amino acid sequence to the reference protein (peptide). It is "substantially structurally identical" if condition (b) applies, regardless of (a).

Percentage amino acid identity is determined by aligning the mutant and reference sequences according to a rigorous dynamic programming algorithm which globally aligns their sequences to maximize their similarity, the similarity being scored as the sum of scores for each aligned pair according to an unbiased PAM250 matrix, and a penalty for each internal gap of -12 for the first null of the gap and -4 for each additional null of the same gap. The percentage identity is the number of matches expressed as a percentage of the adjusted (i.e., counting inserted nulls) length of the reference sequence.

A mutant DNA sequence is substantially identical to a reference DNA sequence if they are structural sequences, and encoding mutant and reference proteins which are substantially identical as described above.

If instead they are regulatory sequences, they are substantially identical if the mutant sequence has at least 10% of the regulatory activity of the reference sequence, and is at least 50% identical in nucleotide sequence to the reference sequence. Percentage identity is determined as for proteins except that matches are scored +5, mismatches -4, the gap open penalty is -12, and the gap extension penalty (per additional null) is -4.

Preferably, sequence which are substantially identical exceed the minimum identity of 50% e.g., are 51%, 66%, 75%, 80%, 85%, 90%, 95% or 99% identical in sequence.

DNA sequences may also be considered "substantially identical" if they hybridize to each other under stringent conditions, i.e., conditions at which the  $T_m$  of the heteroduplex of the one strand of the mutant DNA and the

more complementary strand of the reference DNA is not in excess of 10°C. less than the T<sub>m</sub> of the reference DNA homoduplex. Typically this will correspond to a percentage identity of 85-90%.

5

"Conservative Modifications"

"Conservative modifications" are defined as

- (a) conservative substitutions of amino acids as hereafter defined; or
- 10 (b) single or multiple insertions (extension) or deletions (truncation) of amino acids at the termini.

Conservative modifications are preferred to other modifications. Conservative substitutions are preferred to  
15 other conservative modifications.

"Semi-Conservative Modifications" are modifications which are not conservative, but which are (a) semi-conservative substitutions as hereafter defined; or (b)  
20 single or multiple insertions or deletions internally, but at interdomain boundaries, in loops or in other segments of relatively high mobility. Semi-conservative modifications are preferred to nonconservative modifications. Semi-conservative substitutions are preferred to other semi-conservative modifications.

25 Non-conservative substitutions are preferred to other non-conservative modifications.

The term "conservative" is used here in an a priori sense, i.e., modifications which would be expected to preserve 3D structure and activity, based on analysis of the  
30 naturally occurring families of homologous proteins and of past experience with the effects of deliberate mutagenesis, rather than post facto, a modification already known to conserve activity. Of course, a modification which is conservative a priori may, and usually is, also conservative  
35 post facto.

Preferably, except at the termini, no more than about five amino acids are inserted or deleted at a particular locus, and the modifications are outside regions known to

contain binding sites important to activity.

Preferably, insertions or deletions are limited to the termini.

5 A conservative substitution is a substitution of one amino acid for another of the same exchange group, the exchange groups being defined as follows

- I Gly, Pro, Ser, Ala (Cys) (and any nonbiogenic, neutral amino acid with a hydrophobicity not exceeding that of the aforementioned a.a.'s)
- 10 II Arg, Lys, His (and any nonbiogenic, positively-charged amino acids)
- III Asp, Glu, Asn, Gln (and any nonbiogenic negatively-charged amino acids)
- 15 IV Leu, Ile, Met, Val (Cys) (and any nonbiogenic, aliphatic, neutral amino acid with a hydrophobicity too high for I above)
- V Phe, Trp, Tyr (and any nonbiogenic, aromatic neutral amino acid with a hydrophobicity too high for I above).

20 Note that Cys belongs to both I and IV.

Residues Pro, Gly and Cys have special conformational roles. Cys participates in formation of disulfide bonds. Gly imparts flexibility to the chain. Pro imparts rigidity to the chain and disrupts  $\alpha$  helices. These residues may be essential in certain regions of the polypeptide, but substitutable elsewhere.

One, two or three conservative substitutions are more likely to be tolerated than a larger number.

30 "Semi-conservative substitutions" are defined herein as being substitutions within supergroup I/II/III or within supergroup IV/V, but not within a single one of groups I-V. They also include replacement of any other amino acid with alanine. If a substitution is not conservative, it preferably is semi-conservative.

35 "Non-conservative substitutions" are substitutions which are not "conservative" or "semi-conservative".

"Highly conservative substitutions" are a subset of conservative substitutions, and are exchanges of amino acids

within the groups Phe/Tyr/Trp, Met/Leu/Ile/Val, His/Arg/Lys, Asp/Glu and Ser/Thr/Ala. They are more likely to be tolerated than other conservative substitutions. Again, the smaller the number of substitutions, the more likely they are to be tolerated.

#### "Conservatively Identical"

A protein (peptide) is conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by conservative modifications, the protein (peptide) remaining at least seven amino acids long if the reference protein (peptide) was at least seven amino acids long.

A protein is at least semi-conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by semi-conservative or conservative modifications.

A protein (peptide) is nearly conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by one or more conservative modifications and/or a single nonconservative substitution.

It is highly conservatively identical if it differs, if at all, solely by highly conservative substitutions. Highly conservatively identical proteins are preferred to those merely conservatively identical. An absolutely identical protein is even more preferred.

The core sequence of a reference protein (peptide) is the largest single fragment which retains at least 10% of a particular specific binding activity, if one is specified, or otherwise of at least one specific binding activity of the referent. If the referent has more than one specific binding activity, it may have more than one core sequence, and these may overlap or not.

If it is taught that a peptide of the present invention may have a particular similarity relationship (e.g., markedly identical) to a reference protein (peptide),

preferred peptides are those which comprise a sequence having that relationship to a core sequence of the reference protein (peptide), but with internal insertions or deletions in either sequence excluded. Even more preferred peptides are those whose entire sequence has that relationship, with the same exclusion, to a core sequence of that reference protein (peptide).

## 10 **Library**

The term "library" generally refers to a collection of chemical or biological entities which are related in origin, structure, and/or function, and which can be screened simultaneously for a property of interest.

15 Libraries may be classified by how they are constructed (natural vs. artificial diversity; combinatorial vs. noncombinatorial), how they are screened (hybridization, expression, display), or by the nature of the screened library members (peptides, nucleic acids, etc.).

20 In a "natural diversity" library, essentially all of the diversity arose without human intervention. This would be true, for example, of messenger RNA extracted from a non-engineered cell.

25 In a "synthetic diversity" library, essentially all of the diversity arose deliberately as a result of human intervention. This would be true for example of a combinatorial library; note that a small level of natural diversity could still arise as a result of spontaneous mutation. It would also be true of a noncombinatorial library of compounds collected from diverse sources, even if they were all natural products.

In a "non-natural diversity" library, at least some of the diversity arose deliberately through human intervention.

35 In a "controlled origin" library, the source of the diversity is limited in some way. A limitation might be to cells of a particular individual, to a particular species, or to a particular genus, or, more complexly, to individuals of a particular species who are of a particular age, sex,

physical condition, geographical location, occupation and/or familial relationship. Alternatively or additionally, it might be to cells of a particular tissue or organ. Or it could be cells exposed to particular pharmacological,  
5 environmental, or pathogenic conditions. Or the library could be of chemicals, or a particular class of chemicals, produced by such cells.

In a "controlled structure" library, the library members are deliberately limited by the production  
10 conditions to particular chemical structures. For example, if they are oligomers, they may be limited in length and monomer composition, e.g. hexapeptides composed of the twenty genetically encoded amino acids.

#### 15 Hybridization Library

In a hybridization library, the library members are nucleic acids, and are screened using a nucleic acid hybridization probe. Bound nucleic acids may then be amplified, cloned, and/or sequenced.

#### 20 Expression Library

In an expression library, the screened library members are gene expression products, but one may also speak of an underlying library of genes encoding those products. The  
25 library is made by subcloning DNA encoding the library members (or portions thereof) into expression vectors (or into cloning vectors which subsequently are used to construct expression vectors), each vector comprising an expressible gene encoding a particular library member,  
30 introducing the expression vectors into suitable cells, and expressing the genes so the expression products are produced.

In one embodiment, the expression products are secreted, so the library can be screened using an affinity  
35 reagent, such as an antibody or receptor. The bound expression products may be sequenced directly, or their sequences inferred by, e.g., sequencing at least the variable portion of the encoding DNA.



In a second embodiment, the cells are lysed, thereby exposing the expression products, and the latter are screened with the affinity reagent.

5 In a third embodiment, the cells express the library members in such a manner that they are displayed on the surface of the cells, or on the surface of viral particles produced by the cells. (See display libraries, below).

10 In a fourth embodiment, the screening is not for the ability of the expression product to bind to an affinity reagent, but rather for its ability to alter the phenotype of the host cell in a particular detectable manner. Here, the screened library members are transformed cells, but there is a first underlying library of expression products which mediate the behavior of the cells, and a second  
15 underlying library of genes which encode those products.

#### Display Library

In a display library, the library members are each conjugated to, and displayed upon, a support of some kind.  
20 The support may be living (a cell or virus), or nonliving (e.g., a bead or plate).

If the support is a cell or virus, display will normally be effectuated by expressing a fusion protein which comprises the library member, a carrier moiety allowing  
25 integration of the fusion protein into the surface of the cell or virus, and optionally a lining moiety. In a variation on this theme, the cell coexpresses a first fusion comprising the library member and a linking moiety L1, and a second fusion comprising a linking moiety L2 and the carrier  
30 moiety. L1 and L2 interact to associate the first fusion with the second fusion and hence, indirectly, the library member with the surface of the cell or virus.

#### Soluble Library

35 In a soluble library, the library members are free in solution. A soluble library may be produced directly, or one may first make a display library and then release the library members from their supports.

### Encapsulated Library

In an encapsulated library, the library members are inside cells or liposomes. Generally speaking, encapsulated libraries are used to store the library members for future use; the members are extracted in some way for screening purposes. However, if they differentially affect the phenotype of the cells, they may be screened indirectly by screening the cells.

### 10 cDNA Library

A cDNA library is usually prepared by extracting RNA from cells of particular origin, fractionating the RNA to isolate the messenger RNA (mRNA has a poly(A) tail, so this is usually done by oligo-dT affinity chromatography), synthesizing complementary DNA (cDNA) using reverse transcriptase, DNA polymerase, and other enzymes, subcloning the cDNA into vectors, and introducing the vectors into cells. Often, only mRNAs or cDNAs of particular sizes will be used, to make it more likely that the cDNA encodes a functional polypeptide.

A cDNA library explores the natural diversity of the transcribed DNAs of cells from a particular source. It is not a combinatorial library.

A cDNA library may be used to make a hybridization library, or it may be used as an (or to make) expression library.

### Genomic DNA Library

A genomic DNA library is made by extracting DNA from a particular source, fragmenting the DNA, isolating fragments of a particular size range, subcloning the DNA fragments into vectors, and introducing the vectors into cells.

Like a cDNA library, a genomic DNA library is a natural diversity library, and not a combinatorial library. A genomic DNA library may be used the same way as a cDNA library.

### Synthetic DNA library

A synthetic DNA library may be screened directly (as a hybridization library), or used in the creation of an expression or display library of peptides/proteins.

## 5 Combinatorial Libraries

10 The term "combinatorial library" refers to a library in which the individual members are either systematic or random combinations of a limited set of basic elements, the properties of each member being dependent on the choice and location of the elements incorporated into it. Typically, the members of the library are at least capable of being screened simultaneously. Randomization may be complete or partial; some positions may be randomized and others predetermined, and at random positions, the choices may be limited in a predetermined manner. The members of a combinatorial library may be oligomers or polymers of some kind, in which the variation occurs through the choice of monomeric building block at one or more positions of the oligomer or polymer, and possibly in terms of the connecting linkage, or the length of the oligomer or polymer, too. Or the members may be nonoligomeric molecules with a standard core structure, like the 1,4-benzodiazepine structure, with the variation being introduced by the choice of substituents at particular variable sites on the core structure. Or the members may be nonoligomeric molecules assembled like a jigsaw puzzle, but wherein each piece has both one or more variable moieties (contributing to library diversity) and one or more constant moieties (providing the functionalities for coupling the piece in question to other pieces).

30 Thus, in a typical combinatorial library, chemical building blocks are at least partially randomly combined into a large number (as high as  $10^{15}$ ) of different compounds, which are then simultaneously screened for binding (or other) activity against one or more targets.

35 In a "simple combinatorial library", all of the members belong to the same class of compounds (e.g., peptides) and can be synthesized simultaneously. A "composite combinatorial library" is a mixture of two or more simple

libraries, e.g., DNAs and peptides, or peptides, peptoids, and PNAs, or benzodiazepines and carbamates. The number of component simple libraries in a composite library will, of course, normally be smaller than the average number of members in each simple library, as otherwise the advantage of a library over individual synthesis is small.

Libraries of thousands, even millions, of random oligopeptides have been prepared by chemical synthesis (Houghten et al., *Nature*, 354:84-6(1991)), or gene expression (Marks et al., *J Mol Biol*, 222:581-97(1991)), displayed on chromatographic supports (Lam et al., *Nature*, 354:82-4(1991)), inside bacterial cells (Colas et al., *Nature*, 380:548-550(1996)), on bacterial pili (Lu, *Bio/Technology*, 13:366-372(1990)), or phage (Smith, *Science*, 228:1315-7(1985)), and screened for binding to a variety of targets including antibodies (Valadon et al., *J Mol Biol*, 261:11-22(1996)), cellular proteins (Schmitz et al., *J Mol Biol*, 260:664-677(1996)), viral proteins (Hong and Boulanger, *Embo J*, 14:4714-4727(1995)), bacterial proteins (Jacobsson and Frykberg, *Biotechniques*, 18:878-885(1995)), nucleic acids (Cheng et al., *Gene*, 171:1-8(1996)), and plastic (Siani et al., *J Chem Inf Comput Sci*, 34:588-593(1994)).

Libraries of proteins (Ladner, USP 4,664,989), peptoids (Simon et al., *Proc Natl Acad Sci U S A*, 89:9367-71(1992)), nucleic acids (Ellington and Szostak, *Nature*, 246:818(1990)), carbohydrates, and small organic molecules (Eichler et al., *Med Res Rev*, 15:481-96(1995)) have also been prepared or suggested for drug screening purposes.

The first combinatorial libraries were composed of peptides or proteins, in which all or selected amino acid positions were randomized. Peptides and proteins can exhibit high and specific binding activity, and can act as catalysts. In consequence, they are of great importance in biological systems.

Nucleic acids have also been used in combinatorial libraries. Their great advantage is the ease with which a nucleic acid with appropriate binding activity can be

amplified. As a result, combinatorial libraries composed of nucleic acids can be of low redundancy and hence, of high diversity.

5 There has also been much interest in combinatorial  
libraries based on small molecules, which are more suited to  
pharmaceutical use, especially those which, like  
benzodiazepines, belong to a chemical class which has  
already yielded useful pharmacological agents. The  
10 techniques of combinatorial chemistry have been recognized  
as the most efficient means for finding small molecules that  
act on these targets. At present, small molecule  
combinatorial chemistry involves the synthesis of either  
pooled or discrete molecules that present varying arrays of  
functionality on a common scaffold. These compounds are  
15 grouped in libraries that are then screened against the  
target of interest either for binding or for inhibition of  
biological activity.

The size of a library is the number of molecules in it.  
The simple diversity of a library is the number of unique  
20 structures in it. There is no formal minimum or maximum  
diversity. If the library has a very low diversity, the  
library has little advantage over just synthesizing and  
screening the members individually. If the library is of  
very high diversity, it may be inconvenient to handle, at  
25 least without automatizing the process. The simple  
diversity of a library is preferably at least 10, 10E2,  
10E3, 10E4, 10E6, 10E7, 10E8 or 10E9, the higher the better  
under most circumstances. The simple diversity is usually  
not more than 10E15, and more usually not more than 10E10.

30 The average sampling level is the size divided by the  
simple diversity. The expected average sampling level must  
be high enough to provide a reasonable assurance that, if a  
given structure were expected, as a consequence of the  
library design, to be present, that the actual average  
35 sampling level will be high enough so that the structure, if  
satisfying the screening criteria, will yield a positive  
result when the library is screened. Thus, the preferred  
average sampling level is a function of the detection limit,

which in turn is a function of the strength of the signal to be screened.

There are more complex measures of diversity than simple diversity. These attempt to take into account the degree of structural difference between the various unique sequences. These more complex measures are usually used in the context of small organic compound libraries, see below.

The library members may be presented as solutes in solution, or immobilized on some form of support. In the latter case, the support may be living (cell, virus) or nonliving (bead, plate, etc.). The supports may be separable (cells, virus particles, beads) so that binding and nonbinding members can be separated, or nonseparable (plate). In the latter case, the members will normally be placed on addressable positions on the support. The advantage of a soluble library is that there is no carrier moiety that could interfere with the binding of the members to the support. The advantage of an immobilized library is that it is easier to identify the structure of the members which were positive.

When screening a soluble library, or one with a separable support, the target is usually immobilized. When screening a library on a nonseparable support, the target will usually be labeled.

#### Oligonucleotide Libraries

An oligonucleotide library is a combinatorial library, at least some of whose members, are single-stranded oligonucleotides having three or more nucleotides connected by phosphodiester or analogous bonds. The oligonucleotides may be linear, cyclic or branched, and may include non-nucleic acid moieties. The nucleotides are not limited to the nucleotides normally found in DNA or RNA. For examples of nucleotides modified to increase nuclease resistance and chemical stability of aptamers, see Chart 1 in Osborne and Ellington, Chem. Rev., 97: 349-70 (1997). For screening of RNA, see Ellington and Szostak, Nature, 346: 818-22 (1990).

There is no formal minimum or maximum size for these

oligonucleotides. However, the number of conformations which an oligonucleotide can assume increases exponentially with its length in bases. Hence, a longer oligonucleotide is more likely to be able to fold to adapt itself to a protein surface. On the other hand, while very long molecules can be synthesized and screened, unless they provide a much superior affinity to that of shorter molecules, they are not likely to be found in the selected population, for the reasons explained by Osborne and Ellington (1997). Hence, the libraries of the present invention are preferably composed of oligonucleotides having a length of 3 to 100 bases, more preferably 15 to 35 bases. The oligonucleotides in a given library may be of the same or of different lengths..

Oligonucleotide libraries have the advantage that libraries of very high diversity (e.g.,  $10^{15}$ ) are feasible, and binding molecules are readily amplified in vitro by polymerase chain reaction (PCR). Moreover, nucleic acid molecules can have very high specificity and affinity to targets.

In a preferred embodiment, this invention prepares and screens oligonucleotide libraries by the SELEX method, as described in King and Famulok, *Molec. Biol. Repts.*, 20: 97-107 (1994); L. Gold, C. Tuerk. *Methods of producing nucleic acid ligands*, US#5595877; Oliphant et al. *Gene* 44:177 (1986).

The term "aptamer" is conferred on those oligonucleotides which bind the target protein. Such aptamers may be used to characterize the target protein, both directly (through identification of the aptamer and the points of contact between the aptamer and the protein) and indirectly (by use of the aptamer as a ligand to modify the chemical reactivity of the protein).

In a classic oligonucleotide, each nucleotide (monomeric unit) is composed of a phosphate group, a sugar moiety, and either a purine or a pyrimidine base. In DNA, the sugar is deoxyribose and in RNA it is ribose. The nucleotides are linked by 5'-3' phosphodiester bonds.

The deoxyribose phosphate backbone of DNA can be modified to increase resistance to nuclease and to increase penetration of cell membranes. Derivatives such as mono- or dithiophosphates, methyl phosphonates, boranophosphates, formacetals, carbamates, siloxanes, and dimethylenethio- - sulfoxideo- and-sulfono- linked species are known in the art.

### Peptide Library

A peptide is composed of a plurality of amino acid residues joined together by peptidyl ( $-NHCO-$ ) bonds. A biogenic peptide is a peptide in which the residues are all genetically encoded amino acid residues; it is not necessary that the biogenic peptide actually be produced by gene expression.

Amino acids are the basic building blocks with which peptides and proteins are constructed. Amino acids possess both an amino group ( $-NH_2$ ) and a carboxylic acid group ( $-COOH$ ). Many amino acids, but not all, have the alpha amino acid structure  $NH_2-CHR-COOH$ , where R is hydrogen, or any of a variety of functional groups.

Twenty amino acids are genetically encoded: Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Proline, Serine, Threonine, Tryptophan, Tyrosine, and Valine. Of these, all save Glycine are optically isomeric, however, only the L-form is found in humans. Nevertheless, the D-forms of these amino acids do have biological significance; D-Phe, for example, is a known analgesic.

Many other amino acids are also known, including: 2-Aminoadipic acid; 3-Aminoadipic acid; beta-Aminopropionic acid; 2-Aminobutyric acid; 4-Aminobutyric acid (Piperidinic acid); 6-Aminocaproic acid; 2-Aminoheptanoic acid; 2-Aminoisobutyric acid, 3-Aminoisobutyric acid; 2-Aminopimelic acid; 2,4-Diaminobutyric acid; Desmosine; 2,2'-Diaminopimelic acid; 2,3-Diaminopropionic acid; N-Ethylglycine; N-Ethylasparagine; Hydroxylysine; allo-



Hydroxylysine; 3-Hydroxyproline; 4-Hydroxyproline;  
Isodesmosine; allo-Isoleucine; N-Methylglycine (Sarcosine);  
N-Methylisoleucine; N-Methylvaline; Norvaline; Norleucine;  
and Ornithine.

5           Peptides are constructed by condensation of amino acids  
and/or smaller peptides. The amino group of one amino acid  
(or peptide) reacts with the carboxylic acid group of a  
second amino acid (or peptide) to form a peptide (-NHCO-)  
bond, releasing one molecule of water. Therefore, when an  
10       amino acid is incorporated into a peptide, it should,  
technically speaking, be referred to as an amino acid  
residue. The core of that residue is the moiety which  
excludes the -NH and -CO linking functionalities which  
connect it to other residues. This moiety consists of one  
15       or more main chain atoms (see below) and the attached side  
chains.

          The main chain moiety of each amino acid consists of  
the -NH and -CO linking functionalities and a core main  
chain moiety. Usually the latter is a single carbon atom.  
20       However, the core main chain moiety may include additional  
carbon atoms, and may also include nitrogen, oxygen or  
sulfur atoms, which together form a single chain. In a  
preferred embodiment, the core main chain atoms consist  
solely of carbon atoms.

25           The side chains are attached to the core main chain  
atoms. For alpha amino acids, in which the side chain is  
attached to the alpha carbon, the C-1, C-2 and N-2 of each  
residue form the repeating unit of the main chain, and the  
word "side chain" refers to the C-3 and higher numbered  
30       carbon atoms and their substituents. It also includes H  
atoms attached to the main chain atoms.

          Amino acids may be classified according to the number  
of carbon atoms which appear in the main chain between the  
carbonyl carbon and amino nitrogen atoms which participate  
35       in the peptide bonds. Among the 150 or so amino acids which  
occur in nature, alpha, beta, gamma and delta amino acids  
are known. These have 1-4 intermediary carbons. Only alpha  
amino acids occur in proteins. Proline is a special case of

an alpha amino acid; its side chain also binds to the peptide bond nitrogen.

For beta and higher order amino acids, there is a choice as to which main chain core carbon a side chain other than H is attached to. The preferred attachment site is the C-2 (alpha) carbon, i.e., the one adjacent to the carboxyl carbon of the -CO linking functionality. It is also possible for more than one main chain atom to carry a side chain other than H. However, in a preferred embodiment, only one main chain core atom carries a side chain other than H.

A main chain carbon atom may carry either one or two side chains; one is more common. A side chain may be attached to a main chain carbon atom by a single or a double bond; the former is more common.

A simple combinatorial peptide library is one whose members are peptides having three or more amino acids connected via peptide bonds.

The peptides may be linear, branched, or cyclic, and may covalently or noncovalently include nonpeptidyl moieties. The amino acids are not limited to the naturally occurring or to the genetically encoded amino acids.

A biased peptide library is one in which one or more (but not all) residues of the peptides are constant residues.

### *Cyclic Peptides*

Many naturally occurring peptides are cyclic. Cyclization is a common mechanism for stabilization of peptide conformation thereby achieving improved association of the peptide with its ligand and hence improved biological activity. Cyclization is usually achieved by intra-chain cystine formation, by formation of peptide bond between side chains or between N- and C- terminals. Cyclization was usually achieved by peptides in solution, but several publications have appeared that describe cyclization of peptides on beads.

A peptide library may be an oligopeptide library or a protein library.

### *Oligopeptides*

Preferably, the oligopeptides are at least five, six, seven or eight amino acids in length. Preferably, they are composed of less than 50, more preferably less than 20 amino acids.

In the case of an oligopeptide library, all or just some of the residues may be variable. The oligopeptide may be unconstrained, or constrained to a particular conformation by, e.g., the participation of constant cysteine residues in the formation of a constraining disulfide bond.

### *Proteins*

Proteins, like oligopeptides, are composed of a plurality of amino acids, but the term protein is usually reserved for longer peptides, which are able to fold into a stable conformation. A protein may be composed of two or more polypeptide chains, held together by covalent or noncovalent crosslinks. These may occur in a homooligomeric or a heterooligomeric state.

A peptide is considered a protein if it (1) is at least 50 amino acids long, or (2) has at least two stabilizing covalent crosslinks (e.g., disulfide bonds). Thus, conotoxins are considered proteins.

Usually, the proteins of a protein library will be characterizable as having both constant residues (the same for all proteins in the library) and variable residues (which vary from member to member). This is simply because, for a given range of variation at each position, the sequence space (simple diversity) grows exponentially with the number of residue positions, so at some point it becomes inconvenient for all residues of a peptide to be variable positions. Since proteins are usually larger than oligopeptides, it is more common for protein libraries than oligopeptide libraries to feature variable positions.

In the case of a protein library, it is desirable to focus the mutations at those sites which are tolerant of mutation. These may be determined by alanine scanning

mutagenesis or by comparison of the protein sequence to that of homologous proteins of similar activity. It is also more likely that mutation of surface residues will directly affect binding. Surface residues may be determined by  
5 inspecting a 3D structure of the protein, or by labeling the surface and then ascertaining which residues have received labels. They may also be inferred by identifying regions of high hydrophilicity within the protein.

Because proteins are often altered at some sites but  
10 not others, protein libraries can be considered a special case of the biased peptide library.

There are several reasons that one might screen a protein library instead of an oligopeptide library, including (1) a particular protein, mutated in the library,  
15 has the desired activity to some degree already, and (2) the oligopeptides are not expected to have a sufficiently high affinity or specificity since they do not have a stable conformation.

When the protein library is based on a parental protein  
20 which does not have the desired activity, the parental protein will usually be one which is of high stability (melting point  $\geq 50$  deg. C.) and/or possessed of hypervariable regions.

The variable domains of an antibody possess  
25 hypervariable regions and hence, in some embodiments, the protein library comprises members which comprise a mutant of VH or VL chain, or a mutant of an antigen-specific binding fragment of such a chain. VH and VL chains are usually each about 110 amino acid residues, and are held in proximity by  
30 a disulfide bond between the adjoining CL and CH1 regions to form a variable domain. Together, the VH, VL, CL and CH1 form an Fab fragment.

In human heavy chains, the hypervariable regions are at 31-35, 49-65, 98-111 and 84-88, but only the first three are  
35 involved in antigen binding. There is variation among VH and VL chains at residues outside the hypervariable regions, but to a much lesser degree.

A sequence is considered a mutant of a VH or VL chain

if it is at least 80% identical to a naturally occurring VH or VL chain at all residues outside the hypervariable region.

5 In a preferred embodiment, such antibody library members comprise both at least one VH chain and at least one VL chain, at least one of which is a mutant chain, and which chains may be derived from the same or different antibodies. The VH and VL chains may be covalently joined by a suitable linker moiety, as in a "single chain antibody", or they may  
10 be noncovalently joined, as in a naturally occurring variable domain.

If the joining is noncovalent, and the library is displayed on cells or virus, then either the VH or the VL chain may be fused to the carrier surface/coat protein. The  
15 complementary chain may be co-expressed, or added exogenously to the library.

The members may further comprise some or all of an antibody constant heavy and/or constant light chain, or a mutant thereof.

20

### Peptoid Library

A peptoid is an analogue of a peptide in which one or more of the peptide bonds (-NH-CO-) are replaced by pseudopeptide bonds, which may be the same or different. It  
25 is not necessary that all of the peptide bonds be replaced, i.e., a peptoid may include one or more conventional amino acid residues, e.g., proline.

A peptide bond has two small divalent linker elements, -NH- and -CO-. Thus, a preferred class of pseudopeptide  
30 bonds are those which consist of two small divalent linker elements. Each may be chosen independently from the group consisting of amine (-NH-), substituted amine (-NR-), carbonyl (-CO-), thiocarbonyl (-CS-), methylene (-CH<sub>2</sub>-), monosubstituted methylene (-CHR-), disubstituted methylene (-CR<sub>1</sub>R<sub>2</sub>-), ether (-O-) and thioether (-S-). The more  
35 preferred pseudopeptide bonds include:

N-modified -NRCO-

Carba Ψ -CH<sub>2</sub>-CH<sub>2</sub>-

Depsi  $\Psi$  -CO-O-  
 Hydroxyethylene  $\Psi$  -CHOH-CH<sub>2</sub>-  
 Ketomethylene  $\Psi$  -CO-CH<sub>2</sub>-  
 Methylene-Oxy -CH<sub>2</sub>-O-  
 5 Reduced -CH<sub>2</sub>-NH-  
 Thiomethylene -CH<sub>2</sub>-S-  
 Thiopeptide -CS-NH-  
 Retro-Inverso -CO-NH-

10 A single peptoid molecule may include more than one kind of pseudopeptide bond.

For the purposes of introducing diversity into a peptoid library, one may vary (1) the side chains attached to the core main chain atoms of the monomers linked by the pseudopeptide bonds, and/or (2) the side chains (e.g., the -  
 15 R of an -NRCO-) of the pseudopeptide bonds. Thus, in one embodiment, the monomeric units which are not amino acid residues are of the structure -NR1-CR2-CO-, where at least one of R1 and R2 are not hydrogen. If there is variability  
 20 in the pseudopeptide bond, this is most conveniently done by using an -NRCO- or other pseudopeptide bond with an R group, and varying the R group. In this event, the R group will usually be any of the side chains characterizing the amino acids of peptides, as previously discussed.

25 If the R group of the pseudopeptide bond is not variable, it will usually be small, e.g., not more than 10 atoms (e.g., hydroxyl, amino, carboxyl, methyl, ethyl, propyl).

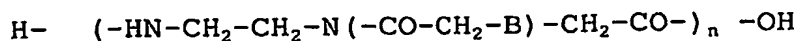
30 If the conjugation chemistries are compatible, a simple combinatorial library may include both peptides and peptoids.

#### Peptide Nucleic Acid Library

35 A PNA oligomer is here defined as one comprising a plurality of units, at least one of which is a PNA monomer which comprises a side chain comprising a nucleobase. For nucleobases, see USP 6,077,835.

The classic PNA oligomer is composed of (2-

aminoethyl)glycine units, with nucleobases attached by methylene carbonyl linkers. That is, it has the structure



where the outer parenthesized substructure is the PNA monomer.

In this structure, the nucleobase B is separated from the backbone N by three bonds, and the points of attachment of the side chains are separated by six bonds. The nucleobase may be any of the bases included in the nucleotides discussed in connection with oligonucleotide libraries. The bases of nucleotides A, G, T, C and U are preferred.

A PNA oligomer may further comprise one or more amino acid residues, especially glycine and proline.

One can readily envision related molecules in which (1) the -COCH<sub>2</sub>- linker is replaced by another linker, especially one composed of two small divalent linkers as defined previously, (2) a side chain is attached to one of the three main chain carbons not participating in the peptide bond (either instead or in addition to the side chain attached to the N of the classic PNA); and/or (3) the peptide bonds are replaced by pseudopeptide bonds as disclosed previously in the context of peptoids.

PNA oligomer libraries have been made; see e.g. Cook, 6,204,326.

### Small Organic Compound Library

The small organic compound library ("compound library", for short) is a combinatorial library whose members are suitable for use as drugs if, indeed, they have the ability to mediate a biological activity of the target protein.

Peptides have certain disadvantages as drugs. These include susceptibility to degradation by serum proteases, and difficulty in penetrating cell membranes. Preferably, all or most of the compounds of the compound library avoid,

or at least do not suffer to the same degree, one or more of the pharmaceutical disadvantages of peptides.

In designing a compound library, it is helpful to bear in mind the methods of molecular modification typically used to obtain new drugs. Three basic kinds of modification may be identified: disjunction, in which a lead drug is simplified to identify its component pharmacophoric moieties; conjunction, in which two or more known pharmacophoric moieties, which may be the same or different, are associated, covalently or noncovalently, to form a new drug; and alteration, in which one moiety is replaced by another which may be similar or different, but which is not in effect a disjunction or conjunction. The use of the terms "disjunction", "conjunction" and "alteration" is intended only to connote the structural relationship of the end product to the original leads, and not how the new drugs are actually synthesized, although it is possible that the two are the same.

The process of disjunction is illustrated by the evolution of neostigmine (1931) and edrophonium (1952) from physostigmine (1925). Subsequent conjunction is illustrated by demecarium (1956) and ambenonium (1956).

Alterations may modify the size, polarity, or electron distribution of an original moiety. Alterations include ring closing or opening, formation of lower or higher homologues, introduction or saturation of double bonds, introduction of optically active centers, introduction, removal or replacement of bulky groups, isosteric or bioisosteric substitution, changes in the position or orientation of a group, introduction of alkylating groups, and introduction, removal or replacement of groups with a view toward inhibiting or promoting inductive (electrostatic) or conjugative (resonance) effects.

Thus, the substituents may include electron acceptors and/or electron donors. Typical electron donors (+I) include  $-\text{CH}_3$ ,  $-\text{CH}_2\text{R}$ ,  $-\text{CHR}_2$ ,  $-\text{CR}_3$  and  $-\text{COO}^-$ . Typical electron acceptors (-I) include  $-\text{NH}_3^+$ ,  $-\text{NR}_3^+$ ,  $-\text{NO}_2$ ,  $-\text{CN}$ ,  $-\text{COOH}$ ,  $-\text{COOR}$ ,  $-\text{CHO}$ ,  $-\text{COR}$ ,  $-\text{COR}$ ,  $-\text{F}$ ,  $-\text{Cl}$ ,  $-\text{Br}$ ,  $-\text{OH}$ ,  $-\text{OR}$ ,  $-\text{SH}$ ,  $-\text{SR}$ ,  $-\text{CH}=\text{CH}_2$ ,



-CR=CR<sub>2</sub>, and -C=CH.

The substituents may also include those which increase or decrease electronic density in conjugated systems. The former (+R) groups include -CH<sub>3</sub>, -CR<sub>3</sub>, -F, -Cl, -Br, -I, -OH, -OR, -OCOR, -SH, -SR, -NH<sub>2</sub>, -NR<sub>2</sub>, and -NHCOR. The later (-R) groups include -NO<sub>2</sub>, -CN, -CHC, -COR, -COOH, -COOR, -CONH<sub>2</sub>, -SO<sub>2</sub>R and -CF<sub>3</sub>.

Synthetically speaking, the modifications may be achieved by a variety of unit processes, including nucleophilic and electrophilic substitution, reduction and oxidation, addition elimination, double bond cleavage, and cyclization.

For the purpose of constructing a library, a compound, or a family of compounds, having one or more pharmacological activities (which need not be related to the known or suspected activities of the target protein), may be disjoined into two or more known or potential pharmacophoric moieties. Analogues of each of these moieties may be identified, and mixtures of these analogues reacted so as to reassemble compounds which have some similarity to the original lead compound. It is not necessary that all members of the library possess moieties analogous to all of the moieties of the lead compound.

The design of a library may be illustrated by the example of the benzodiazepines. Several benzodiazepine drugs, including chlordiazepoxide, diazepam and oxazepam, have been used as anti-anxiety drugs. Derivatives of benzodiazepines have widespread biological activities; derivatives have been reported to act not only as anxiolytics, but also as anticonvulsants; cholecystokinin (CCK) receptor subtype A or B, kappa opioid receptor, platelet activating factor, and HIV transactivator Tat antagonists, and GPIIbIIIa, reverse transcriptase and ras farnesyltransferase inhibitors.

The benzodiazepine structure has been disjoined into a 2-aminobenzophenone, an amino acid, and an alkylating agent. See Bunin, et al., Proc. Nat. Acad. Sci. USA, 91:4708 (1994). Since only a few 2-aminobenzophenone derivatives

are commercially available, it was later disjoined into 2-aminoarylstannane, an acid chloride, an amino acid, and an alkylating agent. Bunin, et al., Meth. Enzymol., 267:448 (1996). The arylstannane may be considered the core structure upon which the other moieties are substituted, or all four may be considered equals which are conjoined to make each library member.

A basic library synthesis plan and member structure is shown in Figure 1 of Fowlkes, et al., U.S. Serial No. 08/740,671, incorporated by reference in its entirety. The acid chloride building block introduces variability at the R<sup>1</sup> site. The R<sup>2</sup> site is introduced by the amino acid, and the R<sup>3</sup> site by the alkylating agent. The R<sup>4</sup> site is inherent in the arylstannane. Bunin, et al. generated a 1, 4-benzodiazepine library of 11,200 different derivatives prepared from 20 acid chlorides, 35 amino acids, and 16 alkylating agents. (No diversity was introduced at R<sup>4</sup>; this group was used to couple the molecule to a solid phase.) According to the Available Chemicals Directory (HDL Information Systems, San Leandro CA), over 300 acid chlorides, 80 Fmoc-protected amino acids and 800 alkylating agents were available for purchase (and more, of course, could be synthesized). The particular moieties used were chosen to maximize structural dispersion, while limiting the numbers to those conveniently synthesized in the wells of a microtiter plate. In choosing between structurally similar compounds, preference was given to the least substituted compound.

The variable elements included both aliphatic and aromatic groups. Among the aliphatic groups, both acyclic and cyclic (mono- or poly-) structures, substituted or not, were tested. (While all of the acyclic groups were linear, it would have been feasible to introduce a branched aliphatic). The aromatic groups featured either single and multiple rings, fused or not, substituted or not, and with heteroatoms or not. The secondary substituents included -NH<sub>2</sub>, -OH, -OMe, -CN, -Cl, -F, and -COOH. While not used, spacer moieties, such as -O-, -S-, -OO-, -CS-, -NH-, and -

NR-, could have been incorporated.

Bunin et al. suggest that instead of using a 1, 4-benzodiazepine as a core structure, one may instead use a 1, 4-benzodiazepine-2, 5-dione structure.

5 As noted by Bunin et al., it is advantageous, although not necessary, to use a linkage strategy which leaves no trace of the linking functionality, as this permits construction of a more diverse library.

10 Other combinatorial nonoligomeric compound libraries known or suggested in the art have been based on carbamates, mercaptoacylated pyrrolidines, phenolic agents, aminimides, N-acylamino ethers (made from amino alcohols, aromatic hydroxy acids, and carboxylic acids), N-alkylamino ethers (made from aromatic hydroxy acids, amino alcohols and  
15 aldehydes) 1, 4-piperazines, and 1, 4-piperazine-6-ones.

DeWitt, et al., Proc. Nat. Acad. Sci. (USA), 90:6909-13 (1993) describe the simultaneous but separate, synthesis of 40 discrete hydantoins and 40 discrete benzodiazepines. They carry out their synthesis on a solid support (inside a  
20 gas dispersion tube), in an array format, as opposed to other conventional simultaneous synthesis techniques (e.g., in a well, or on a pin). The hydantoins were synthesized by first simultaneously deprotecting and then treating each of five amino acid resins with each of eight isocyanates. The  
25 benzodiazepines were synthesized by treating each of five deprotected amino acid resins with each of eight 2-amino benzophenone imines.

Chen, et al., J. Am. Chem. Soc., 116:2661-62 (1994) described the preparation of a pilot (9 member)  
30 combinatorial library of formate esters. A polymer bead-bound aldehyde preparation was "split" into three aliquots, each reacted with one of three different ylide reagents. The reaction products were combined, and then divided into three new aliquots, each of which was reacted with a  
35 different Michael donor. Compound identity was found to be determinable on a single bead basis by gas chromatography/mass spectroscopy analysis.

Holmes, USP 5,549,974 (1996) sets forth methodologies

for the combinatorial synthesis of libraries of thiazolidinones and metathiazanones. These libraries are made by combination of amines, carbonyl compounds, and thiols under cyclization conditions.

5 Ellman, USP 5,545,568 (1996) describes combinatorial synthesis of benzodiazepines, prostaglandins, beta-turn mimetics, and glycerol-based compounds. See also Ellman, USP 5,288,514.

10 Summerton, USP 5,506,337 (1996) discloses methods of preparing a combinatorial library formed predominantly of morpholino subunit structures.

Heterocyclic combinatorial libraries are reviewed generally in Nefzi, et al., Chem. Rev., 97:449-472 (1997).

15 For pharmacological classes, see, e.g., Goth, Medical Pharmacology: Principles and Concepts (C.V. Mosby Co.: 8th ed. 1976); Korolkovas and Burckhalter, Essentials of Medicinal Chemistry (John Wiley & Sons, Inc.: 1976). For synthetic methods, see, e.g., Warren, Organic Synthesis: The  
20 Disconnection Approach (John Wiley & Sons, Ltd.: 1982); Fuson, Reactions of Organic Compounds (John Wiley & Sons: 1966); Payne and Payne, How to do an Organic Synthesis (Allyn and Bacon, Inc.: 1969); Greene, Protective Groups in Organic Synthesis (Wiley-Interscience). For selection of  
25 substituents, see e.g., Hansch and Leo, Substituent Constants for Correlation Analysis in Chemistry and Biology (John Wiley & Sons: 1979).

The library is preferably synthesized so that the individual members remain identifiable so that, if a member  
30 is shown to be active, it is not necessary to analyze it. Several methods of identification have been proposed, including:

- (1) encoding, i.e., the attachment to each member of an identifier moiety which is more readily  
35 identified than the member proper. This has the disadvantage that the tag may itself influence the activity of the conjugate.
- (2) spatial addressing, e.g., each member is

synthesized only at a particular coordinate on or in a matrix, or in a particular chamber. This might be, for example, the location of a particular pin, or a particular well on a microtiter plate, or inside a "tea bag".

The present invention is not limited to any particular form of identification.

However, it is possible to simply characterize those members of the library which are found to be active, based on the characteristic spectroscopic indicia of the various building blocks.

Solid phase synthesis permits greater control over which derivatives are formed. However, the solid phase could interfere with activity. To overcome this problem, some or all of the molecules of each member could be liberated, after synthesis but before screening.

Examples of candidate simple libraries which might be evaluated include derivatives of the following:

Cyclic Compounds Containing One Hetero Atom

Heteronitrogen

pyrroles

pentasubstituted pyrroles

pyrrolidines

pyrrolines

prolines

indoles

beta-carbolines

pyridines

dihydropyridines

1,4-dihydropyridines

pyrido[2,3-d]pyrimidines

tetrahydro-3H-imidazo[4,5-c] pyridines

Isoquinolines

tetrahydroisoquinolines

quinolones

beta-lactams

azabicyclo[4.3.0]nonen-8-one amino acid

Heterooxygen

	furans
	tetrahydrofurans
	2,5-disubstituted tetrahydrofurans.
	pyrans
5	hydroxypyranones
	tetrahydroxypyranones
	gamma-butyrolactones
	Heterosulfur
	sulfolenes
10	Cyclic Compounds with Two or More Hetero atoms
	Multiple heteronitrogens
	imidazoles
	pyrazoles
	piperazines
15	diketopiperazines
	arylpiperazines
	benzylpiperazines
	benzodiazepines
	1,4-benzodiazepine-2,5-diones
20	hydantoins
	5-alkoxyhydantoins
	dihydropyrimidines
	1,3-disubstituted-5,6-dihydropyrimidine-2,4-
25	diones
	cyclic ureas
	cyclic thioureas
	quinazolines
	chiral 3-substituted-quinazoline-2,4-
30	diones
	triazoles
	1,2,3-triazoles
	purines
	Heteronitrogen and Heterooxygen
35	dikelomorpholines
	isoxazoles
	isoxazolines
	Heteronitrogen and Heterosulfur

thiazolidines

N-axylthiazolidines

dihydrothiazoles

2-methylene-2,3-dihydrothiazates

5

2-aminothiazoles

thiophenes

3-amino thiophenes

4-thiazolidinones

4-melathiazanones

10

benzisothiazolones

For details on synthesis of libraries, see Nefzi, et al., Chem. Rev., 97:449-72 (1997), and references cited therein.

15

#### **Pharmaceutical Methods and Preparations**

20

The preferred animal subject of the present invention is a mammal. By the term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects, although it is intended for veterinary and nutritional uses as well. Preferred nonhuman subjects are of the orders Primata (e.g., apes and monkeys), Artiodactyla or Perissodactyla (e.g., cows, pigs, sheep, horses, goats), Carnivora (e.g., cats, dogs), Rodenta (e.g., rats, mice, guinea pigs, hamsters), Lagomorpha (e.g., rabbits) or other pet, farm or laboratory mammals.

25

The term "protection", as used herein, is intended to include "prevention," "suppression" and "treatment." "Prevention", strictly speaking, involves administration of the pharmaceutical prior to the induction of the disease (or other adverse clinical condition). "Suppression" involves administration of the composition prior to the clinical appearance of the disease. "Treatment" involves administration of the protective composition after the appearance of the disease.

35

It will be understood that in human and veterinary medicine, it is not always possible to distinguish between "preventing" and "suppressing" since the ultimate inductive

event or events may be unknown, latent, or the patient is not ascertained until well after the occurrence of the event or events. Therefore, unless qualified, the term "prevention" will be understood to refer to both prevention in the strict sense, and to suppression.

The preventative or prophylactic use of a pharmaceutical involves identifying subjects who are at higher risk than the general population of contracting the disease, and administering the pharmaceutical to them in advance of the clinical appearance of the disease. The effectiveness of such use is measured by comparing the subsequent incidence or severity of the disease, or of particular symptoms of the disease, in the treated subjects against that in untreated subjects of the same high risk group.

While high risk factors vary from disease to disease, in general, these include (1) prior occurrence of the disease in one or more members of the same family, or, in the case of a contagious disease, in individuals with whom the subject has come into potentially contagious contact at a time when the earlier victim was likely to be contagious, (2) a prior occurrence of the disease in the subject, (3) prior occurrence of a related disease, or a condition known to increase the likelihood of the disease, in the subject; (4) appearance of a suspicious level of a marker of the disease, or a related disease or condition; (5) a subject who is immunologically compromised, e.g., by radiation treatment, HIV infection, drug use, etc., or (6) membership in a particular group (e.g., a particular age, sex, race, ethnic group, etc.) which has been epidemiologically associated with that disease.

A prophylaxis or treatment may be curative, that is, directed at the underlying cause of a disease, or ameliorative, that is, directed at the symptoms of the disease, especially those which reduce the quality of life.

It should also be understood that to be useful, the protection provided need not be absolute, provided that it is sufficient to carry clinical value. An agent which



provides protection to a lesser degree than do competitive agents may still be of value if the other agents are ineffective for a particular individual, if it can be used in combination with other agents to enhance the level of protection, or if it is safer than competitive agents. It is desirable that there be a statistically significant ( $p=0.05$  or less) improvement in the treated subject relative to an appropriate untreated control, and it is desirable that this improvement be at least 10%, more preferably at least 25%, still more preferably at least 50%, even more preferably at least 100%, in some indicia of the incidence or severity of the disease or of at least one symptom of the disease.

At least one of the drugs of the present invention may be administered, by any means that achieve their intended purpose, to protect a subject against a disease or other adverse condition. The form of administration may be systemic or topical. For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. Parenteral administration can be by bolus injection or by gradual perfusion over time.

A typical regimen comprises administration of an effective amount of the drug, administered over a period ranging from a single dose, to dosing over a period of hours, days, weeks, months, or years.

It is understood that the suitable dosage of a drug of the present invention will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. However, the most preferred dosage can be tailored to the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation. This will typically involve adjustment of a standard dose, e.g., reduction of the dose if the patient has a low body weight.

Prior to use in humans, a drug will first be evaluated

for safety and efficacy in laboratory animals. In human clinical studies, one would begin with a dose expected to be safe in humans, based on the preclinical data for the drug in question, and on customary doses for analogous drugs (if any). If this dose is effective, the dosage may be decreased, to determine the minimum effective dose, if desired. If this dose is ineffective, it will be cautiously increased, with the patients monitored for signs of side effects. See, e.g., Berkow et al, eds., *The Merck Manual*, 15th edition, Merck and Co., Rahway, N.J., 1987; Goodman et al., eds., *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, 8th edition, Pergamon Press, Inc., Elmsford, N.Y., (1990); Avery's *Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics*, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, MD. (1987), Ebadi, *Pharmacology*, Little, Brown and Co., Boston, (1985), which references and references cited therein, are entirely incorporated herein by reference.

The total dose required for each treatment may be administered by multiple doses or in a single dose. The protein may be administered alone or in conjunction with other therapeutics directed to the disease or directed to other symptoms thereof.

~~Typical pharmaceutical doses, for adult humans, are in the range of 1 mg to 100 mg per day, more often 1 mg to 10 mg per day.~~

The appropriate dosage form will depend on the disease, the pharmaceutical, and the mode of administration; possibilities include tablets, capsules, lozenges, dental pastes, suppositories, inhalants, solutions, ointments and parenteral depots. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, including all references cited therein.

In the case of peptide drugs, the drug may be administered in the form of an expression vector comprising a nucleic acid encoding the peptide; such a vector, after incorporation into the genetic complement of a cell of the

patient, directs synthesis of the peptide. Suitable vectors include genetically engineered poxviruses (vaccinia), adenoviruses, adeno-associated viruses, herpesviruses and lentiviruses which are or have been rendered nonpathogenic..

5 In addition to at least one drug as described herein, a pharmaceutical composition may contain suitable pharmaceutically acceptable carriers, such as excipients, carriers and/or auxiliaries which facilitate processing of the active compounds into preparations which can be used  
10 pharmaceutically. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, included all references cited therein.

#### 15 **Assay Compositions and Methods**

##### Target Organism

The invention contemplates that it may be appropriate to ascertain or to mediate the biological activity of a substance of this invention in a target organism.

20 The target organism may be a plant, animal, or microorganism.

In the case of a plant, it may be an economic plant, in which case the drug may be intended to increase the disease, weather or pest resistance, alter the growth  
25 characteristics, or otherwise improve the useful characteristics or mute undesirable characteristics of the plant. Or it may be a weed, in which case the drug may be intended to kill or otherwise inhibit the growth of the plant, or to alter its characteristics to convert it from a  
30 weed to an economic plant. The plant may be a tree, shrub, crop, grass, etc. The plant may be an algae (which are in some cases also microorganisms), or a vascular plant, especially gymnosperms (particularly conifers) and angiosperms. Angiosperms may be monocots or dicots. The  
35 plants of greatest interest are rice, wheat, corn, alfalfa, soybeans, potatoes, peanuts, tomatoes, melons, apples, pears, plums, pineapples, fir, spruce, pine, cedar, and oak.

If the target organism is a microorganism, it may be

algae, bacteria, fungi, or a virus (although the biological activity of a virus must be determined in a virus-infected cell). The microorganism may be human or other animal or plant pathogen, or it may be nonpathogenic. It may be a  
5 soil or water organism, or one which normally lives inside other living things.

If the target organism is an animal, it may be a vertebrate or a nonvertebrate animal. Nonvertebrate animals are chiefly of interest when they act as pathogens or  
10 parasites, and the drugs are intended to act as biocidal or biostatic agents. Nonvertebrate animals of interest include worms, mollusks, and arthropods.

The target organism may also be a vertebrate animal, i.e., a mammal, bird, reptile, fish or amphibian. Among  
15 mammals, the target animal preferably belongs to the order Primata (humans, apes and monkeys), Artiodactyla (e.g., cows, pigs, sheep, goats, horses), Rodenta (e.g., mice, rats) Lagomorpha (e.g., rabbits, hares), or Carnivora (e.g., cats, dogs). Among birds, the target animals are preferably  
20 of the orders Anseriformes (e.g., ducks, geese, swans) or Galliformes (e.g., quails, grouse, pheasants, turkeys and chickens). Among fish, the target animal is preferably of the order Clupeiformes (e.g., sardines, shad, anchovies, whitefish, salmon).

#### Target Tissues

The term "target tissue" refers to any whole animal, physiological system, whole organ, part of organ, miscellaneous tissue, cell, or cell component (e.g., the  
30 cell membrane) of a target animal in which biological activity may be measured.

Routinely in mammals one would choose to compare and contrast the biological impact on virtually any and all tissues which express the subject receptor protein. The  
35 main tissues to use are: brain, heart, lung, kidney, liver, pancreas, skin, intestines, adipose, stomach, skeletal muscle, adrenal glands, breast, prostate, vasculature, retina, cornea, thyroid gland, parathyroid glands, thymus,

bone marrow, bone, etc.

Another classification would be by cell type: B cells, T cells, macrophages, neutrophils, eosinophils, mast cells, platelets, megakaryocytes, erythrocytes, bone marrow stomal  
5 cells, fibroblasts, neurons, astrocytes, neuroglia, microglia, epithelial cells (from any organ, e.g. skin, breast, prostate, lung, intestines etc), cardiac muscle cells, smooth muscle cells, striated muscle cells, osteoblasts, osteocytes, chondroblasts, chondrocytes,  
10 keratinocytes, melanocytes, etc.

Of course, in the case of a unicellular organism, there is no distinction between the "target organism" and the "target tissue".

#### 15 Screening Assays

Assays intended to determine the binding or the biological activity of a substance are called preliminary screening assays.

Screening assays will typically be either in vitro  
20 (cell-free) assays (for binding to an immobilized receptor) or cell-based assays (for alterations in the phenotype of the cell). They will not involve screening of whole multicellular organisms, or isolated organs. The comments on diagnostic biological assays apply mutatis mutandis to  
25 screening cell-based assays.

#### In Vitro vs. In Vivo Assays

The term *in vivo* is descriptive of an event, such as binding or enzymatic action, which occurs within a living  
30 organism. The organism in question may, however, be genetically modified. The term *in vitro* refers to an event which occurs outside a living organism. Parts of an organism (e.g., a membrane, or an isolated biochemical) are used, together with artificial substrates and/or conditions.  
35 For the purpose of the present invention, the term *in vitro* excludes events occurring inside or on an intact cell, whether of a unicellular or multicellular organism.

In vivo assays include both cell-based assays, and

organismic assays. The cell-based assays include both assays on unicellular organisms, and assays on isolated cells or cell cultures derived from multicellular organisms. The cell cultures may be mixed, provided that they are not organized into tissues or organs. The term organismic assay refers to assays on whole multicellular organisms, and assays on isolated organs or tissues of such organisms.

#### In vitro Diagnostic Methods and Reagents

The in vitro assays of the present invention may be applied to any suitable analyte-containing sample, and may be qualitative or quantitative in nature.

#### *Sample*

The sample will normally be a biological fluid, such as blood, urine, lymph, semen, milk, or cerebrospinal fluid, or a fraction or derivative thereof, or a biological tissue, in the form of, e.g., a tissue section or homogenate. However, the sample conceivably could be (or derived from) a food or beverage, a pharmaceutical or diagnostic composition, soil, or surface or ground water. If a biological fluid or tissue, it may be taken from a human or other mammal, vertebrate or animal, or from a plant. The preferred sample is blood, or a fraction or derivative thereof.

#### *Binding and Reaction Assays*

The assay may be a binding assay, in which one step involves the binding of a diagnostic reagent to the analyte, or a reaction assay, which involves the reaction of a reagent with the analyte. The reagents used in a binding assay may be classified as to the nature of their interaction with analyte: (1) analyte analogues, or (2) analyte binding molecules (ABM). They may be labeled or insolubilized.

In a reaction assay, the assay may look for a direct reaction between the analyte and a reagent which is reactive with the analyte, or if the analyte is an enzyme or enzyme

inhibitor, for a reaction catalyzed or inhibited by the analyte. The reagent may be a reactant, a catalyst, or an inhibitor for the reaction.

5 An assay may involve a cascade of steps in which the product of one step acts as the target for the next step. These steps may be binding steps, reaction steps, or a combination thereof.

#### *Signal Producing System (SPS)*

10 In order to detect the presence, or measure the amount, of an analyte, the assay must provide for a signal producing system (SPS) in which there is a detectable difference in the signal produced, depending on whether the analyte is  
15 present or absent (or, in a quantitative assay, on the amount of the analyte). The detectable signal may be one which is visually detectable, or one detectable only with instruments. Possible signals include production of colored or luminescent products, alteration of the characteristics  
20 (including amplitude or polarization) of absorption or emission of radiation by an assay component or product, and precipitation or agglutination of a component or product. The term "signal" is intended to include the discontinuance of an existing signal, or a change in the rate of change of  
25 an observable parameter, rather than a change in its absolute value. The signal may be monitored manually or automatically.

30 In a reaction assay, the signal is often a product of the reaction. In a binding assay, it is normally provided by a label borne by a labeled reagent.

#### *Labels*

35 The component of the signal producing system which is most intimately associated with the diagnostic reagent is called the "label". A label may be, e.g., a radioisotope, a fluorophore, an enzyme, a co-enzyme, an enzyme substrate, an electron-dense compound, an agglutinable particle.

The radioactive isotope can be detected by such means

as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention include  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$  and  $^{33}\text{P}$ .  $^{125}\text{I}$  is preferred for antibody labeling.

The label may also be a fluorophore. When the fluorescently labeled reagent is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, *o*-phthaldehyde and fluorescamine.

Alternatively, fluorescence-emitting metals such as  $^{125}\text{Eu}$ , or others of the lanthanide series, may be incorporated into a diagnostic reagent using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The label may also be a chemiluminescent compound. The presence of the chemiluminescently labeled reagent is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isolumino, therrromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used for labeling. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Enzyme labels, such as horseradish peroxidase and alkaline phosphatase, are preferred. When an enzyme label is used, the signal producing system must also include a substrate for the enzyme. If the enzymatic reaction product is not itself detectable, the SPS will include one or more additional reactants so that a detectable product appears.



An enzyme analyte may act as its own label if an enzyme inhibitor is used as a diagnostic reagent.

#### *Binding Assay Formats*

5 Binding assays may be divided into two basic types, heterogeneous and homogeneous. In heterogeneous assays, the interaction between the affinity molecule and the analyte does not affect the label, hence, to determine the amount or presence of analyte, bound label must be separated from free  
10 label. In homogeneous assays, the interaction does affect the activity of the label, and therefore analyte levels can be deduced without the need for a separation step.

In one embodiment, the ABM is insolubilized by coupling it to a macromolecular support, and analyte in the sample is  
15 allowed to compete with a known quantity of a labeled or specifically labelable analyte analogue. The "analyte analogue" is a molecule capable of competing with analyte for binding to the ABM, and the term is intended to include analyte itself. It may be labeled already, or it may be  
20 labeled subsequently by specifically binding the label to a moiety differentiating the analyte analogue from analyte. The solid and liquid phases are separated, and the labeled analyte analogue in one phase is quantified. The higher the level of analyte analogue in the solid phase, i.e.,  
25 sticking to the ABM, the lower the level of analyte in the sample.

In a "sandwich assay", both an insolubilized ABM, and a labeled ABM are employed. The analyte is captured by the insolubilized ABM and is tagged by the labeled ABM, forming  
30 a ternary complex. The reagents may be added to the sample in either order, or simultaneously. The ABMs may be the same or different. The amount of labeled ABM in the ternary complex is directly proportional to the amount of analyte in the sample.

35 The two embodiments described above are both heterogeneous assays. However, homogeneous assays are conceivable. The key is that the label be affected by whether or not the complex is formed.

### Conjugation Methods

A label may be conjugated, directly or indirectly (e.g., through a labeled anti-ABM antibody), covalently (e.g., with SPDP) or noncovalently, to the ABM, to produce a  
5 diagnostic reagent. Similarly, the ABM may be conjugated to a solid phase support to form a solid phase ("capture") diagnostic reagent.

Suitable supports include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases,  
10 natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention.

The support material may have virtually any possible  
15 structural configuration so long as the coupled molecule is capable of binding to its target. Thus the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may  
20 be flat such as a sheet, test strip, etc.

### Biological Assays

A biological assay measures or detects a biological response of a biological entity to a substance.

25 The biological entity may be a whole organism, an isolated organ or tissue, freshly isolated cells, an immortalized cell line, or a subcellular component (such as a membrane; this term should not be construed as including an isolated receptor). The entity may be, or may be derived  
30 from, an organism which occurs in nature, or which is modified in some way. Modifications may be genetic (including radiation and chemical mutants, and genetic engineering) or somatic (e.g., surgical, chemical, etc.).  
35 In the case of a multicellular entity, the modifications may affect some or all cells. The entity need not be the target organism, or a derivative thereof, if there is a reasonable correlation between bioassay activity in the assay entity and biological activity in the target organism.

The entity is placed in a particular environment, which may be more or less natural. For example, a culture medium may, but need not, contain serum or serum substitutes, and it may, but need not, include a support matrix of some kind, it may be still, or agitated. It may contain particular biological or chemical agents, or have particular physical parameters (e.g., temperature), that are intended to nourish or challenge the biological entity.

There must also be a detectable biological marker for the response. At the cellular level, the most common markers are cell survival and proliferation, cell behavior (clustering, motility), cell morphology (shape, color), and biochemical activity (overall DNA synthesis, overall protein synthesis, and specific metabolic activities, such as utilization of particular nutrients, e.g., consumption of oxygen, production of CO<sub>2</sub>, production of organic acids, uptake or discharge of ions).

The direct signal produced by the biological marker may be transformed by a signal producing system into a different signal which is more observable, for example, a fluorescent or colorimetric signal.

The entity, environment, marker and signal producing system are chosen to achieve a clinically acceptable level of sensitivity, specificity and accuracy.

In some cases, the goal will be to identify substances which mediate the biological activity of a natural biological entity, and the assay is carried out directly with that entity. In other cases, the biological entity is used simply as a model of some more complex (or otherwise inconvenient to work with) biological entity. In that event, the model biological entity is used because activity in the model system is considered more predictive of activity in the ultimate natural biological entity than is simple binding activity in an in vitro system. The model entity is used instead of the ultimate entity because the former is more expensive or slower to work with, or because ethical considerations forbid working with the ultimate entity yet.

The model entity may be naturally occurring, if the model entity usefully models the ultimate entity under some conditions. Or it may be non-naturally occurring, with modifications that increase its resemblance to the ultimate entity.

Transgenic animals, such as transgenic mice, rats, and rabbits, have been found useful as model systems.

In cell-based model assays, where the biological activity is mediated by binding to a receptor (target protein), the receptor may be functionally connected to a signal (biological marker) producing system, which may be endogenous or exogenous to the cell.

There are a number of techniques of doing this:

#### 15 "Zero-Hybrid" Systems

In these systems, the binding of a peptide to the target protein results in a screenable or selectable phenotypic change, without resort to fusing the target protein (or a ligand binding moiety thereof) to an endogenous protein. It may be that the target protein is endogenous to the host cell, or is substantially identical to an endogenous receptor so that it can take advantage of the latter's native signal transduction pathway. Or sufficient elements of the signal transduction pathway normally associated with the target protein may be engineered into the cell so that the cell signals binding to the target protein.

#### "One-Hybrid" Systems

In these systems, a chimera receptor, a hybrid of the target protein and an endogenous receptor, is used. The chimeric receptor has the ligand binding characteristics of the target protein and the signal transduction characteristics of the endogenous receptor. Thus, the normal signal transduction pathway of the endogenous receptor is subverted.

Preferably, the endogenous receptor is inactivated, or the conditions of the assay avoid activation of the

endogenous receptor, to improve the signal-to-noise ratio.

See Fowlkes USP 5,789,184 for a yeast system.

Another type of "one-hybrid" system combines a peptide:  
DNA-binding domain fusion with an unfused target receptor  
5 that possesses an activation domain.

#### "Two-Hybrid" System

In a preferred embodiment, the cell-based assay is a  
two hybrid system. This term implies that the ligand is  
10 incorporated into a first hybrid protein, and the receptor  
into a second hybrid protein. The first hybrid also  
comprises component A of a signal generating system, and the  
second hybrid comprises component B of that system.  
Components A and B, by themselves, are insufficient to  
15 generate a signal. However, if the ligand binds the  
receptor, components A and B are brought into sufficiently  
close proximity so that they can cooperate to generate a  
signal.

Components A and B may naturally occur, or be  
20 substantially identical to moieties which naturally occur,  
as components of a single naturally occurring biomolecule,  
or they may naturally occur, or be substantially identical  
to moieties which naturally occur, as separate naturally  
occurring biomolecules which interact in nature.

25

#### Two-Hybrid System: Transcription Factor Type

In a preferred "two-hybrid" embodiment, one member of a  
peptide ligand:receptor binding pair is expressed as a  
fusion to a DNA-binding domain (DBD) from a transcription  
30 factor (this fusion protein is called the "bait"), and the  
other is expressed as a fusion to a transactivation domain  
(TAD) (this fusion protein is called the "fish", the "prey",  
or the "catch"). The transactivation domain should be  
complementary to the DNA-binding domain, i.e., it should  
35 interact with the latter so as to activate transcription of  
a specially designed reporter gene that carries a binding  
site for the DNA-binding domain. Naturally, the two fusion  
proteins must likewise be complementary.

This complementarity may be achieved by use of the complementary and separable DNA-binding and transcriptional activator domains of a single transcriptional activator protein, or one may use complementary domains derived from  
5 different proteins. The domains may be identical to the native domains, or mutants thereof. The assay members may be fused directly to the DBD or TAD, or fused through an intermediated linker.

The target DNA operator may be the native operator  
10 sequence, or a mutant operator. Mutations in the operator may be coordinated with mutations in the DBD and the TAD. An example of a suitable transcription activation system is one comprising the DNA-binding domain from the bacterial repressor LexA and the activation domain from the yeast  
15 transcription factor Gal4, with the reporter gene operably linked to the LexA operator.

It is not necessary to employ the intact target receptor; just the ligand-binding moiety is sufficient.

The two fusion proteins may be expressed from the same  
20 or different vectors. Likewise, the activatable reporter gene may be expressed from the same vector as either fusion protein (or both proteins), or from a third vector.

Potential DNA-binding domains include Gal4, LexA, and mutant domains substantially identical to the above.

25 Potential activation domains include E. coli B42, Gal4 activation domain II, and HSV VP16, and mutant domains substantially identical to the above.

Potential operators include the native operators for the desired activation domain, and mutant domains  
30 substantially identical to the native operator.

The fusion proteins may comprise nuclear localization signals.

The assay system will include a signal producing system, too. The first element of this system is a reporter  
35 gene operably linked to an operator responsive to the DBD and TAD of choice. The expression of this reporter gene will result, directly or indirectly, in a selectable or screenable phenotype (the signal). The signal producing

system may include, besides the reporter gene, additional genetic or biochemical elements which cooperate in the production of the signal. Such an element could be, for example, a selective agent in the cell growth medium. There may be more than one signal producing system, and the system may include more than one reporter gene.

The sensitivity of the system may be adjusted by, e.g., use of competitive inhibitors of any step in the activation or signal production process, increasing or decreasing the number of operators, using a stronger or weaker DBD or TAD, etc.

When the signal is the death or survival of the cell in question, or proliferation or nonproliferation of the cell in question, the assay is said to be a selection. When the signal merely results in a detectable phenotype by which the signaling cell may be differentiated from the same cell in a nonsignaling state (either way being a living cell), the assay is a screen. However, the term "screening assay" may be used in a broader sense to include a selection. When the narrower sense is intended, we will use the term "nonselective screen".

Various screening and selection systems are discussed in Ladner, USP 5,198,346.

Screening and selection may be for or against the peptide: target protein or compound:target protein interaction.

Preferred assay cells are microbial (bacterial, yeast, algal, protozoal), invertebrate, vertebrate (esp. mammalian, particularly human). The best developed two-hybrid assays are yeast and mammalian systems.

Normally, two hybrid assays are used to determine whether a protein X and a protein Y interact, by virtue of their ability to reconstitute the interaction of the DBD and the TAD. However, augmented two-hybrid assays have been used to detect interactions that depend on a third, non-protein ligand.

For more guidance on two-hybrid assays, see Brent and Finley, Jr., Ann. Rev. Genet., 31:663-704 (1997); Fremont-

Racine, et al., *Nature Genetics*, 277-281 (16 July 1997); Allen, et al., *TIBS*, 511-16 (Dec. 1995); LeCrenier, et al., *BioEssays*, 20:1-6 (1998); Xu, et al., *Proc. Nat. Acad. sci. (USA)*, 94:12473-8 (Nov. 1992); Esotak, et al., *Mol. Cell. Biol.*, 15:5820-9 (1995); Yang, et al., *Nucleic Acids Res.*, 23:1152-6 (1995); Bendixen, et al., *Nucleic Acids Res.*, 22:1778-9 (1994); Fuller, et al., *BioTechniques*, 25:85-92 (July 1998); Cohen, et al., *PNAS (USA)* 95:14272-7 (1998); Kolonin and Finley, Jr., *PNAS (USA)* 95:14266-71 (1998). See also Vasavada, et al., *PNAS (USA)*, 88:10686-90 (1991) (contingent replication assay), and Rehrauer, et al., *J. Biol. Chem.*, 271:23865-73 (1996) (LexA repressor cleavage assay).

#### 15 Two-Hybrid Systems: reporter Enzyme type

In another embodiment, the components A and B reconstitute an enzyme which is not a transcription factor.

As in the last example, the effect of the reconstitution of the enzyme is a phenotypic change which may be a screenable change, a selectable change, or both.

#### In vivo Diagnostic Uses

Radio-labeled ABM may be administered to the human or animal subject. Administration is typically by injection, e.g., intravenous or arterial or other means of administration in a quantity sufficient to permit subsequent dynamic and/or static imaging using suitable radio-detecting devices. The dosage is the smallest amount capable of providing a diagnostically effective image, and may be determined by means conventional in the art, using known radio-imaging agents as a guide.

Typically, the imaging is carried out on the whole body of the subject, or on that portion of the body or organ relevant to the condition or disease under study. The amount of radio-labeled ABM accumulated at a given point in time in relevant target organs can then be quantified.

A particularly suitable radio-detecting device is a



scintillation camera, such as a gamma camera. A scintillation camera is a stationary device that can be used to image distribution of radio-labeled ABM. The detection device in the camera senses the radioactive decay, the distribution of which can be recorded. Data produced by the imaging system can be digitized. The digitized information can be analyzed over time discontinuously or continuously. The digitized data can be processed to produce images, called frames, of the pattern of uptake of the radio-labeled ABM in the target organ at a discrete point in time. In most continuous (dynamic) studies, quantitative data is obtained by observing changes in distributions of radioactive decay in target organs over time. In other words, a time-activity analysis of the data will illustrate uptake through clearance of the radio-labeled binding protein by the target organs with time.

Various factors should be taken into consideration in selecting an appropriate radioisotope. The radioisotope must be selected with a view to obtaining good quality resolution upon imaging, should be safe for diagnostic use in humans and animals, and should preferably have a short physical half-life so as to decrease the amount of radiation received by the body. The radioisotope used should preferably be pharmacologically inert, and, in the quantities administered, should not have any substantial physiological effect.

The ABM may be radio-labeled with different isotopes of iodine, for example  $^{123}\text{I}$ ,  $^{125}\text{I}$ , or  $^{131}\text{I}$  (see for example, U.S. Patent 4,609,725). The extent of radio-labeling must, however be monitored, since it will affect the calculations made based on the imaging results (i.e. a diiodinated ABM will result in twice the radiation count of a similar monoiodinated ABM over the same time frame).

In applications to human subjects, it may be desirable to use radioisotopes other than  $^{125}\text{I}$  for labeling in order to decrease the total dosimetry exposure of the human body and to optimize the detectability of the labeled molecule (though this radioisotope can be used if circumstances

require). Ready availability for clinical use is also a factor. Accordingly, for human applications, preferred radio-labels are for example,  $^{99m}\text{Tc}$ ,  $^{67}\text{Ga}$ ,  $^{68}\text{Ga}$ ,  $^{90}\text{Y}$ ,  $^{111}\text{In}$ ,  $^{113m}\text{In}$ ,  $^{123}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$  or  $^{211}\text{At}$ .

5       The radio-labeled ABM may be prepared by various methods. These include radio-halogenation by the chloramine - T method or the lactoperoxidase method and subsequent purification by HPLC (high pressure liquid chromatography), for example as described by J. Gutkowska et al in  
10       "Endocrinology and Metabolism Clinics of America: (1987) 16 (1):183. Other known methods of radio-labeling can be used, such as IODOBEADS™.

      There are a number of different methods of delivering the radio-labeled ABM to the end-user. It may be  
15       administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. Because proteins are subject to being digested when administered orally, parenteral administration, i.e., intravenous, subcutaneous, intramuscular, would ordinarily  
20       be used to optimize absorption of an ABM, such as an antibody, which is a protein.

## EXAMPLES

### 25       Animal Models.

      Obesity and subsequent hyperinsulinemia and hyperglycemia were induced by feeding a group of 3 week old mice (50 males) a high-fat diet (Bio-Serv, Frenchtown, NJ, F1850 High Carbohydrate-High Fat). Another group of 3 week  
30       old mice (20 males) were fed the normal control diet (PMI Nutrition International Inc., Brentwood, MO, Prolab RMH3000). The mice were placed onto the respective diets immediately following weaning. Animal weights were determined weekly. Fasting blood-glucose and plasma insulin  
35       measurements were determined after 2, 4, 8 and 16 weeks on the respective diets.

      Normal weight, normal fasting blood glucose and normal fasting plasma insulin levels are defined as the respective

mean values of the animals fed the control diet.

Two of the "most typical" animals were selected for each group (Control, hyperinsulinemic and Diabetic) at each time point ( 2,4, 8, and 16 weeks after commencement of diet) for sacrifice. The selected mice were sacrificed and liver tissue obtained and frozen in liquid nitrogen until processed for RNA isolation.

#### **Fasting Blood Glucose Levels.**

Blood glucose levels was measured from a drop of blood taken from the tip of the tail of fasted (6 hr) mice using a Lifescan Genuine One Touch glucometer. All measurements occurred between 3:00 pm and 5:00 pm.

#### **Plasma insulin measurements.**

Blood was collected from the tail of fasted (6hr) mice into a heparinized capillary tube and stored on ice. All collections occurred between 3:00 pm and 5:00 pm. Plasma was separated from red blood cells by centrifugation for 10 minutes at 8000 x g and then stored at -20°C. Insulin concentrations were determined using the Rat Insulin ELISA kit and rat insulin standards (ALPCO) essentially as instructed by the manufacturer. Values were adjusted by a factor of 1.23 as determined by the manufacturer to correct for the species difference in cross-reactivity with the antibody.

#### **RNA isolation.**

Total RNA was isolated from livers using the RNA STAT-60 Total RNA/mRNA Isolation Reagent according to the manufacturer's instructions (Tel-Test, Friendswood, TX).

#### **Sample Quantification and Quality Assessment**

Total RNA was quantified and assessed for quality on a Bioanalyzer RNA 6000 Nano chip (Agilent). Each chip contained an interconnected set of gel-filled channels that allowed for molecular sieving of nucleic acids. Pin-

electrodes in the chip were used to create electrokinetic forces capable of driving molecules through these micro-channels to perform electrophoretic separations. Ribosomal peaks were measured by fluorescence signal and displayed in an electropherogram. A successful total RNA sample featured 2 distinct ribosomal peaks (18S and 28S rRNA).

#### **Biotinylated cRNA Hybridization Target.**

Total RNA was prepared for use as a hybridization target as described in the manufacturer's instructions for CodeLink Expression Bioarrays(TM) (Amersham Biosciences). The CodeLink Expression Bioarrays utilize nucleic acid hybridization of a biotin-labeled complementary RNA(cRNA) target with DNA oligonucleotide probes attached to a gel matrix.

The biotin-labeled cRNA target is prepared by a linear amplification method. Poly (A) + RNA (within the total RNA population) is primed for reverse transcription by a DNA oligonucleotide containing a T7 RNA polymerase promoter 5' to a (dT) 24 sequence. After second-strand cDNA synthesis, the cDNA serves as the template in an *in vitro* transcription (IVT) reaction to produce the target cRNA. The IVT is performed in the presence of biotinylated nucleotides to label the target cRNA. This procedure results in a 50-200 fold linear amplification of the input poly (A) + RNA.

#### **Hybridization Probes.**

The oligonucleotide probes were provided by the Codelink Uniset Mouse I Bioarray (Amersham, product code 300013). Amine-terminated oligonucleotide probes are attached to a three-dimensional polyacrylamide gel matrix. There are 10,000 oligonucleotide probes, each specific to a well-characterized mouse gene. Each mouse gene is representative of a unique gene cluster from the fourth quarter 2001 Genbank Unigene build. There are also 500 control probes.

The sequences of the probes is proprietary to Amersham. However, for each probe, Amersham identifies the

corresponding mouse gene by NCBI accession number, OGS, LocusLink, Unigene Cluster ID, and description (name). This information should be available from Amersham. In the case of the differentially expressed probes, this information is duplicated in master table 1. For the complete list, see [http://www4.amershambiosciences.com/aptrix/upp01077.nsf/Content/codelink\\_literature](http://www4.amershambiosciences.com/aptrix/upp01077.nsf/Content/codelink_literature)

- 10 Under "Gene Lists", select "Uniset Human I", and a gene list, in Excel format, can be downloaded.

### Hybridization

- 15 Using the cRNA target, the hybridization reaction mixture is prepared and loaded until array chambers for bioarray processing as set forth in the manufacturer's instructions for CodeLink Gene Expression Bioarrays™ (Amersham Biosciences). Each sample is hybridized to an individual microarray. Hybridization is at 37°C. The hybridization buffer is prepared as set forth in the Motorola instructions. Hybridization to the microarray is detected with an avidinated fluorescent reagent, Streptavidin-Alexa Fluor ® 647 (Amersham).

### 25 Mouse Gene Expression Analysis

- Processed arrays were scanned using a GenePix 4000B Microarray Scanner (Axon Instruments, Inc.); array images were acquired using the Amersham CodeLink™ Analysis Software (Release 2.2). The Amersham CodeLink™ Analysis Software gives an integrated optical density (IOD) value for every spot; a unique background value for that spot is subtracted, resulting in "raw" data points. Individual chips are then normalized by the Amersham CodeLink™ software according to the median raw intensity for all 10,000 genes. A negative control threshold is also calculated according to the control probes. A significant difference in expression between samples was defined as a minimum of 2-fold change in expression values. Genes with expression values below the

negative control threshold were eliminated from the analysis and then the expression data was analyzed to identify genes whose expression levels changed significantly with respect to:

5

Normal mice compared to hyperinsulinemic mice at 2, 4, 8 and 16 on normal vs. high-fat diet.

10

Normal mice compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 on normal vs. high-fat diet.

Hyperinsulinemic compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 on high-fat diets.

15

**Database Searches** Nucleotide sequences and predicted amino acid sequences were compared to public domain databases using the Blast 2.0 program (National Center for Biotechnology Information, National Institutes of Health). Nucleotide sequences were displayed using ABI prism Edit View 1.0.1 (PE Applied Biosystems, Foster City, CA).

Nucleotide database searches were conducted with the then current version of BLASTN 2.0.12, see Altschul, et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res., 25:3389-3402 (1997). Searches employed the default parameters, unless otherwise stated.

For blastN searches, the default was the blastN matrix (1,-3), with gap penalties of 5 for existence and 2 for extension.

Protein database searches were conducted with the then-current version of BLAST X, see Altschul et al. (1997), supra. Searches employed the default parameters, unless otherwise stated. The scoring matrix was BLOSUM62, with gap costs of 11 for existence and 1 for extension. The standard low complexity filter was used.

"ref" indicates that NCBI's RefSeq is the source database. The identifier that follows is a RefSeq accession

number, not a GenBank accession number. "RefSeq sequences are derived from GenBank and provide non-redundant curated data representing our current knowledge of known genes. Some records include additional sequence information that was never submitted to an archival database but is available in the literature. A small number of sequences are provided through collaboration; the underlying primary sequence data is available in GenBank, but may not be available in any one GenBank record. RefSeq sequences are not submitted primary sequences. RefSeq records are owned by NCBI and therefore can be updated as needed to maintain current annotation or to incorporate additional sequence information." See also <http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>

It will be appreciated by those in the art that the exact results of a database search will change from day to day, as new sequences are added. Also, if you query with a longer version of the original sequence, the results will change. The results given here were obtained at one time and no guarantee is made that the exact same hits would be obtained in a search on the filing date. However, if an alignment between a particular query sequence and a particular database sequence is discussed, that alignment should not change (if the parameters and sequences remain unchanged).

#### **Northern Analysis.**

Northern analysis may be used to confirm the results. Favorable and unfavorable genes, identified as described above, or fragments thereof, will be used as probes in Northern hybridization analyses to confirm their differential expression. Total RNA isolated from Control, Hyperinsulinemic and Type-II Diabetic mice will be resolved by agarose gel electrophoresis through a 1% agarose, 1 % formaldehyde denaturing gel, transferred to positively charged nylon membrane, and hybridized to a probe labeled with [32P] dCTP that was generated from the aforementioned

gene or fragment using the Random Primed DNA Labeling Kit (Roche, Palo Alto, CA).

#### **Real-Time RNA Analysis.**

5        Real-time RNA analysis may also be used for confirmation. For "real-time" RNA analysis, RNA will be converted to cDNA and then probed with gene-specific primers made for each clone. "Real-time" incorporation of fluorescent dye will be measured to determine the amount of  
10       specific transcript present in each sample. Sample differences (control vs. hyperinsulinemic, hyperinsulinemic vs. diabetic, or control vs. diabetic) of 2-fold or greater (in either direction) will be considered differentially expressed. Confirmation using several independent animals  
15       is desirable.

#### **In situ Hybridization**

Another form of confirmation may be provided by nonisotopic *in situ* hybridizations (NISH) on selected human  
20       (obtained by Tissue Informatics) and mouse tissues using cRNA probes generated from mouse genes found to be up- or down-regulated during the disease progression. Nonisotopic *in situ* hybridizations may also be performed on mouse tissues using cRNA probes generated from all "novel" cDNA's  
25       identified through PCR subtractive hybridizations. These cRNA's will hybridize to their corresponding messenger RNA's present in cells and will provide information regarding the particular cell types within a tissue that is expressing the particular gene as well as the relative level of gene  
30       expression. The cRNA probes may be generated by *in vitro* transcription of template cDNA by Sp6 or T7 RNA polymerase in the presence of digoxigenin-11-UTP (Roche Molecular Biochemicals, Mannheim, Germany; Pardue, M.L. 1985. In: *In situ hybridization, Nucleic acid hybridization, a practical*  
35       approach: IRL Press, Oxford, 179-202).

#### **Transgenic Animals.**



Transgenic expression may be used to confirm the results. In one embodiment, a mouse is engineered to overexpress the favorable or unfavorable mouse gene in question. In another embodiment, a mouse is engineered to express the  
5 corresponding favorable or unfavorable human gene. In a third embodiment, a nonhuman animal other than a mouse, such as a rat, rabbit, goat, sheep or pig, is engineered to express the favorable or unfavorable mouse or human gene.

#### 10 **Hyperquantitative Tissue Analysis**

In addition to gene expression analysis the liver sections can also be analyzed using TissueInformatics, Inc's TissueAnalytics™ software. A single representative section may be cut from each liver block, placed on a slide, and  
15 stained with H&E. Digital images of each slide may be acquired using an research microscope and digital camera (Olympus E600 microscope and Sony DKC-ST5). These images were acquired at 20x magnification with a resolution of 0.64 mm/pixel. A hyperquantitative analysis may be performed on  
20 the resulting images: First a digital image analysis can identify and annotate structural objects in a tissue using machine vision. These objects, that are constituents of the tissue, can be annotated because they are visually identifiable and have a biological meaning like hepatocytes,  
25 sinusoids, vacuoles. Subsequently a quantification of these structures regarding their geometric properties like area or stain intensities and their relationship to the field of view or per unit area in terms of a % coverage may be performed. Features or parameters for hyper-quantification  
30 are specific for each tissue, and may also include relations between features, measures of overall heterogeneity, including orientation, relative locations, and textures.

#### **Correlation Analysis**

35 Mathematical statistics provides a rich set of additional tools to analyze time resolved data sets of hyper-quantitative and gene expression profiles for similarities, including rank correlation, the calculation of regression

and correlations coefficients, and clustering. Continuous functions may also be fitted through the data points of individual gene and tissue feature data. Relation between gene expression and hyper-quantitative tissue data may be linear or non-linear, in synchronous or asynchronous arrangements.

A Spearman rank correlation analysis using was done on the 2 classes of measurements (Genes and Tissues Features) to help identify other significant genes. A small number of genes that did not meet the 2-Fold difference for significance were added to the list of genes based on their correlation with tissue features.

Citation of documents herein is not intended as an admission that any of the documents cited herein is pertinent prior art, or an admission that the cited documents is considered material to the patentability of any of the claims of the present application. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicant and does not constitute any admission as to the correctness of the dates or contents of these documents.

The appended claims are to be treated as a non-limiting recitation of preferred embodiments.

In addition to those set forth elsewhere, the following references are hereby incorporated by reference, in their most recent editions as of the time of filing of this application: Kay, Phage Display of Peptides and Proteins: A Laboratory Manual; the John Wiley and Sons Current Protocols series, including Ausubel, Current Protocols in Molecular Biology; Coligan, Current Protocols in Protein Science; Coligan, Current Protocols in Immunology; Current Protocols in Human Genetics; Current Protocols in Cytometry; Current Protocols in Pharmacology; Current Protocols in Neuroscience; Current Protocols in Cell Biology; Current Protocols in Toxicology; Current Protocols in Field Analytical Chemistry; Current Protocols in Nucleic Acid Chemistry; and Current Protocols in Human Genetics; and the following Cold Spring Harbor Laboratory publications: Sambrook, Molecular Cloning: A Laboratory Manual; Harlow, Antibodies: A Laboratory Manual; Manipulating the Mouse Embryo: A Laboratory Manual; Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual; Drosophila Protocols; Imaging Neurons: A Laboratory Manual; Early Development of *Xenopus laevis*: A Laboratory Manual; Using Antibodies: A Laboratory Manual; At the Bench: A Laboratory Navigator; Cells: A Laboratory Manual; Methods in Yeast Genetics: A Laboratory Course Manual; Discovering Neurons: The Experimental Basis of Neuroscience; Genome Analysis: A Laboratory Manual Series ; Laboratory DNA Science; Strategies for Protein Purification and Characterization: A

Laboratory Course Manual; Genetic Analysis of Pathogenic Bacteria: A Laboratory Manual; PCR Primer: A Laboratory Manual; Methods in Plant Molecular Biology: A Laboratory Course Manual ; Manipulating the Mouse Embryo: A Laboratory Manual; Molecular Probes of the Nervous System; Experiments with Fission Yeast: A Laboratory Course Manual; A Short Course in Bacterial Genetics: A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria; DNA Science: A First Course in Recombinant DNA Technology; Methods in Yeast Genetics: A Laboratory Course Manual; Molecular Biology of Plants: A Laboratory Course Manual.

All references cited herein, including journal articles or abstracts, published, corresponding, prior or otherwise related U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology

or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

5       Any description of a class or range as being useful or preferred in the practice of the invention shall be deemed a description of any subclass (e.g., a disclosed class with one or more disclosed members omitted) or subrange contained therein, as well as a separate description of each  
10       individual member or value in said class or range.

      The description of preferred embodiments individually shall be deemed a description of any possible combination of such preferred embodiments, except for combinations which are impossible (e.g, mutually exclusive choices for an  
15       element of the invention) or which are expressly excluded by this specification.

      If an embodiment of this invention is disclosed in the prior art, the description of the invention shall be deemed to include the invention as herein disclosed with such  
20       embodiment excised.

## Introduction to Master Tables

The master tables reflect applicants' analysis of the gene chip data.

5

For each probe corresponding to a differentially expressed mouse gene, Master Table 1 identifies

10

Col. 1: The mouse gene (upper) and mouse protein (lower) database accession #s.

Col. 2: The corresponding mouse Unigene Cluster, as of the 4<sup>th</sup> Quarter 2001 build.

15

Col. 3: The behavior (differential expression) observed for the mouse gene. This column identifies the gene as favorable(F) or unfavorable (U) on the basis of its differential behavior. There are three possible comparisons, HI-D, C-HI, and C-D, where C=control (normal), HI=hyperinsulinemic, and D=diabetic.

20

If the level of the gene in the former state is at least two-fold that in the latter state, it is considered unfavorable. If the level of the gene in the former state is not more than half (i.e., not more than negative two fold) that in the latter state, it is considered favorable.

25

Col. 4: A related human protein, identified by its database accession number. Usually, several such proteins are identified relative to each mouse gene. These proteins have been identified by BLAST searches, as explained in cols. 6-8.

30

Col. 5: The name of the related human protein.

35

Col. 6: The score (in bits) for the alignment performed by the BLAST program.

Col. 7: The E-value for the alignment performed by the BLAST program. It is worth noting that Unigene considers a Blastx E Value of less than  $1e-6$  to be a "match" to the reference sequence of a cluster.

5

Col. 8: The BLAST search strategy used. MG indicates that the mouse gene was used as the query sequence in a BlastX search. MP means that the mouse protein was used as the query sequence in a BlastP search. HGP means that first the mouse gene was used in a BlastN search for a human gene, and then the human gene was used in a BLASTX search for the human protein.

10

15

Master Table 1 is divided into three subtables on the basis of the Behavior" in col. 3. If a gene has at least one favorable behavior, and no unfavorable ones, it is put into Subtable 1A. In the opposite case, it is put into Subtable 1B. If its behavior is mixed, i.e., at least one favorable and at least one unfavorable, it is put into Subtable 1C.

20

Master Table 2 has just three columns.

25

Col. 1: Mouse gene.

Col. 2: behavior. Same as col. 3 in Master table 1.

30

Col. 3: Human protein classes. Based on the related human proteins defined in Master Table 1, Master Table 2 generalizes, if possible as to classes of human proteins which are expected to have similar behavior. For a given mouse gene, several human protein classes may be listed because of the diversity of the human proteins found to be related. In some cases, the stated human protein classes may be hierarchial, e.g., one may be a subset of another. In other cases, the stated classes may be non-overlapping but related. And in yet other cases, the stated classes may be

35

non-overlapping and unrelated. Combinations of the above are also possible.

5 In addition to the classes stated, the corresponding human gene clusters are also of interest. These may be obtained in a number of ways. First, one may search on Unigene (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>) for the identified human protein. Review the "hits" (each of which is a Unigene record) for those prefixed by "Hs."

10 Secondly, one may access the Unigene record for the mouse gene cluster (which is given in Master Table 1), and then click on "Homologene". This will bring up a new page which includes the section "Possible Homologous Genes". One of the entries should be a Homo sapiens gene (considered by

15 Unigene to be the most related human gene); click on its Unigene record link.

Additional information of interest may be accessed by searching with the mouse gene accession # in the Mouse Gene Informatics database, at <http://www.informatics.jax.org/>.

20



**MASTER TABLE 1: Mouse Gene/Human Protein Correlations**  
**Subtable 1A - Favorable**

Mouse Gene Protein	Unigene	Behavior	Human Protein	Human Protein Name	Score	E-Value	BLASTx
NM_007630 NP_031656.1	Mm.22592	F:(HI-D) -5.28	NP_004692.1	cyclin B2	694	0	MG
			NP_114172.1	cyclin B1; G2/mitotic-specific cyclin B1	382	1.00e-106	MG
			XP_172630.1	similar to cyclin B2	239	6.00e-63	MG
NM_007913 NP_031939.1	Mm.181959	F:(HI-D) -2.66	NP_001955.1	early growth response 1; G0S30	783	0	MG
			XP_005040.2	similar to Early growth response protein 3 (EGR-3) (Zinc finger protein pilot)	275	3.00e-73	MG
			NP_004421.1	early growth response 3	274	6.00e-73	MG
AF127033 AAG02285.1	Mm.3760	F:(HI-D) -2.1	NP_004095.3	fatty acid synthase	3961	0	MG
			G01880	fatty-acid synthase (EC 2.3.1.85) (version 2)	3945	0	MG
			P49327	Fatty acid synthase [Includes: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]	3778	0	MG
			B57788	fatty-acid synthase (EC 2.3.1.85) (HepG2 cell variant)	3740	0	MG
			AAH07267.1	Unknown (protein for IMAGE:3138929)	1533	0	MG
			AAB35516.1	fatty acid synthase; FAS [Homo sapiens]	728	0	MG
			AAH07305.1	Unknown (protein for MGC:15708)	685	0	MG
			AAH14634.1	Unknown (protein for IMAGE:3535581)	553	1.00e-156	MG
NM_011169 NP_035299.1	Mm.2752	F:(HI-D) -2.08	NP_000940.1	prolactin receptor	789	0	MG
			AAK32703.1	prolactin receptor isoform delta S1 precursor	605	1.00e-173	MG
			AAL23915.1	prolactin receptor short isoform 1a	512	1.00e-145	MG
			AAD49855.1	intermediate prolactin receptor isoform	509	1.00e-144	MG
			AAL23914.1	prolactin receptor short isoform 1b	448	1.00e-125	MG

AF04772 5 AAD1372 0.1	Mm.421 00	F:(H-I-D) -2.06	NP_00076 3.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	704	0	MG
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	704	0	MG
			NP_00076 0.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	683	0	MG
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	681	0	MG
			AAH2059 6.1	Unknown (protein for MGC:22146)	680	0	MG
			NP_00076 2.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	679	0	MG
			AAB2386 4.2	cytochrome P-450 [Homo sapiens]	679	0	MG
			AAA5216 1.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	679	0	MG
			BAA0012 3.1	cytochrome P-450 [Homo sapiens]	679	0	MG
			NP_00076 1.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	678	0	MG
			S66382	cytochrome P450 2C8 - human.	677	0	MG
			AAB3529 2.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	677	0	MG
			AAA5216 0.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	677	0	MG
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19	676	0	MG
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	674	0	MG
			AAA5215 7.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	674	0	MG
			I506290A	cytochrome P450	674	0	MG
			I52418	cytochrome P450 - human	640	0	MG
NM_0134 90 NP_0385 18.1	Mm.526 2	F:(H-I-D) -2.04	AAH3647 1.1	Similar to choline kinase	679	0	MG
			NP_00126 8.1	choline kinase	665	0	MG
			NP_00518 9.2	choline/ethanolamine kinase isoform a	433	1.00e- 121	MG

5	NM_013888 NP_038916.1	Mm.32550	F:(HI-D) -2.04	NP_068572.1	J domain containing protein 1	310	3.00e-84	MG	
	NM_019499 NP_062372.1	Mm.43444	F:(HI-D) -2.04	NP_002349.1	MAD2-like 1; MAD2 (mitotic arrest deficient, yeast, homolog)-like 1; mitotic arrest deficient, yeast, homolog-like 1	382	1.00e-106	MG	
				21465465	Chain A, Crystal Structure Of Mad1-Mad2 Reveals A Conserved Mad2 Binding Motif In Mad1 And Cdc20	380	1.00e-102	MG	
				18655665	Chain A, The Mad2 Spindle Checkpoint Protein Undergoes Similar Major Conformational Changes Upon Binding To Either Mad1 Or Cdc20	368	1.00e-102	MG	
				7245371	Chain A, Solution Structure Of The Spindle Assembly Checkpoint Protein Human Mad2	348	5.00e-96	MG	
10									
15	NM_011850 NP_035980.1	Mm.34209	F:(HI-D) -2.03	NP_068804.1	short heterodimer partner; orphan nuclear receptor SHP; small heterodimer partner; nuclear receptor subfamily 0, group B, member 2	404	1.00e-112	MG	
				AAC41998.1	nuclear hormone receptor	402	1.00e-112	MG	
20	AF213393 AAF31432.1	Mm.38377	F:(HI-D) -2.02	NP_009099.1	ATP-binding cassette, sub-family A member 8	280	2.00e-75	MG	
				NP_525022.1	ATP-binding cassette, sub-family A (ABC1), member 9	267	2.00e-71	MG	
				AAN32751.1	ATP-binding cassette sub-family A member 9	267	2.00e-71	MG	
25				NP_525021.1	ATP-binding cassette, sub-family A (ABC1), member 10	244	8.00e-65	MG	
				AAM77557.1	ABC transporter ABCA6	227	2.00e-59	MG	
				NP_525023.1	ATP-binding cassette, sub-family A (ABC1), member 6	227	2.00e-59	MG	
30				BAC04994.1	unnamed protein product	227	2.00e-59	MG	
				CAB93535.3	ATP-binding cassette protein	199	3.00e-51	MG	
				NP_061142.1	ATP-binding cassette protein of the (ABCA subfamily)	199	3.00e-51	MG	
35				BAB71700.1	unnamed protein product	199	3.00e-51	MG	
				BAB67781.1	KIAA1888 protein	199	3.00e-51	MG	
				BAB71208.1	unnamed protein product	199	7.00e-51	MG	
	NM_013646 NP_038674.1	Mm.8858	F:(HI-D) -2.02	NP_599023.1	RAR-related orphan receptor A, isoform a; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	954	0	MG	
				NP_002934.1	RAR-related orphan receptor A, isoform c; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0	MG	

			NP_59902 2.1	RAR-related orphan receptor A, isoform b; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0	MG
			NP_59902 4.1	RAR-related orphan receptor A, isoform d; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0	MG
			A56856	retinoid-related orphan receptor RZR-alpha - human	893	0	MG
			NP_00884 5.2	RAR-related orphan receptor B; RAR-related orphan receptor beta; retinoic acid-binding receptor beta; nuclear receptor RZR-beta	561	1.00e- 160	MG
5			CAD1327 6.1	bA133M9.1 (RAR-related orphan receptor B)	561	1.00e- 159	MG
			Q92753	NUCLEAR RECEPTOR ROR-BETA (NUCLEAR RECEPTOR RZR-BETA)	559	1.00e- 159	MG
	NM_0094 25 NP_0334 51.1	Mm.106 2 F:(H-D) -10.21	NP_00380 1.1	tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related apoptosis inducing ligand TRAIL	345	9.00e- 95	MG
10			6980394	Chain A, Crystal Structure Of Apo2/TRAIL	266	4.00e- 71	MG
			6435529	Chain B, Crystal Structure Of Trail-Dr5 Complex	248	2.00e- 65	MG
			10835510	Chain D, Crystal Structure Of Trail-Sdr5	248	2.00e- 65	MG
	NM_0081 82 NP_0322 08.1	Mm.197 422 F:(C-HI) -9.17, F:(C-D) -5.68	NP_66568 3.1	glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2	328	8.00e- 90	MG
15			I52381	glutathione transferase (EC 2.5.1.18) - human	327	1.00e- 89	MG
			DAA0007 1.1	TPA: glutathione transferase A5	327	1.00e- 89	MG
20			442977	Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)	326	3.00e- 89	MG
			I127144	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k)	325	6.00e- 89	MG
			XP_16710 0.2	similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha)	325	6.00e- 89	MG
			Q16772	Glutathione S-transferase A3-3 (GST class-alpha)	324	1.00e- 88	MG
			NP_00083 8.2	glutathione S-transferase A3	322	3.00e- 88	MG
25			A49365	glutathione transferase (EC 2.5.1.18) alpha-3 [similarity] - human	322	4.00e- 88	MG
			AAA7463 4.1	glutathione S-transferase A3	322	4.00e- 88	MG
			S20331	glutathione transferase (EC 2.5.1.18) - human	318	5.00e- 87	MG
			S27110	glutathione transferase (EC 2.5.1.18) A2 - human	317	1.00e- 86	MG
			S24330	thione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human	316	3.00e- 66	MG

			NP_00083 7.2	thione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-alkyltransferase A2; GST-gamma; HA subunit 2	315	4.00e-86	MG	
			CAB9277 0.1	dJ152L7.3 (glutathione S-transferase A2)	315	4.00e-88	MG	
			S77958	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2 (+)) - human	309	3.00e-84	MG	
			A56801	glutathione transferase (EC 2.5.1.18) alpha y - human	309	4.00e-84	MG	
5	NM_028089 NP_082365.1	Mm.142581 F:(C-HI) -4.31, F:(C-D) -5.26	NP_00076 3.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	766	0	MG	
10			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	764	0	MG	
			AAB2386 4.2	cytochrome P-450	736	0	MG	
			NP_00076 2.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	736	0	MG	
			BAA0012 3.1	cytochrome P-450	736	0	MG	
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	729	0	MG	
15			AAA5215 7.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	729	0	MG	
			226295	cytochrome P450	728	0	MG	
			NP_00076 0.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	726	0	MG	
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	722	0	MG	
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	709	0	MG	
20			AAH2059 6.1	Unknown (protein for MGC:22146)	707	0	MG	
			AAA5216 0.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	706	0	MG	
			NP_00076 1.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	706	0	MG	
			S66382	cytochrome P450 2C8 - human	704	0	MG	
			AAB3529 2.1	cytochrome P450 arachidonic acid epoxygenase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	704	0	MG	
			AAA5216 1.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	696	0	MG	

			I52418	cytochrome P450 - human	682	0	MG	
			G38462	chrome P450 2C17 - human (fragment)	593	1.00e-169	MG	
5	NM_007818 NP_031844.1	Mm.21193 F:(C-HI) -4.29, F:(C-D) -8.15	NP_000768.1	cytochrome P450, subfamily IIIA, polypeptide 5; nifedipine oxidase; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase	726	0	MG	
			NP_059488.2	cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3	724	0	MG	
			P08684	Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP3A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)	723	0	MG	
10			NP_000767.1	cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3	723	0	MG	
			AAA35744.1	cytochrome P-450 nifedipine oxidase	722	0	MG	
			AAF13598.1	cytochrome P450-3A4	715	0	MG	
			AAA35747.1	cytochrome P450 nifedipine oxidase	711	0	MG	
			NP_000756.1	cytochrome P450, subfamily IIIA, polypeptide 7; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	698	0	MG	
15			AAG48618.1	cytochrome P450 variant 3A7	693	0	MG	
			NP_476436.1	cytochrome P450 polypeptide 43 isoform 2; cytochrome P450 polypeptide 43	644	0	MG	
			NP_073731.1	cytochrome P450 polypeptide 43 isoform 1; cytochrome P450 polypeptide 43	639	0	MG	
			NP_476437.1	cytochrome P450 polypeptide 43 isoform 3; cytochrome P450 polypeptide 43	525	1.00e-149	MG	
			AAG33012.1	cytochrome P450 subfamily IIIA polypeptide 43	284	2.00e-76	MG	
20			AAF99272.1	thromboxane synthase	278	1.00e-74	MG	
			AAF99279.1	thromboxane synthase	278	2.00e-74	MG	
			AAF99274.1	thromboxane synthase	277	3.00e-74	MG	
			AAF99278.1	thromboxane synthase	277	3.00e-74	MG	
			AAF99276.1	thromboxane synthase	277	4.00e-74	MG	
25			NP_001052.1	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V), isoform TXS-1; TXA synthase	277	4.00e-74	MG	
			AAF99275.1	thromboxane synthase	277	4.00e-74	MG	
			P24557	Thromboxane-A synthase (TXA synthase) (TXS)	276	5.00e-74	MG	
			S48161	thromboxane-A synthase (EC 5.3.99.5) - human	276	5.00e-74	MG	
			BAA07011.1	thromboxane synthase	276	8.00e-74	MG	
			AAF99273.1	thromboxane synthase	275	1.00e-73	MG	

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			AAF9927 7.1	thromboxane synthase	275	1.00e-73	MG	
			AAH1411 7.1	Unknown (protein for MGC:20885)	248	2.00e-65	MG	
			NP_11224 6.1	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V), isoform TXS-II; TXA synthase	204	4.00e-52	MG	
NM_0254 29 NP_0797 05.1	Mm.463 16	F:(C-HI) -3.51, F:(C-D) -3.01	NP_10959 1.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	498	1.00e-140	MG	
			NP_00414 6.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)	276	6.00e-74	MG	
			NP_00501 5.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)	275	1.00e-73	MG	
			NP_00263 1.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	275	2.00e-73	MG	
			NP_00455 9.2	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	272	1.00e-72	MG	
			A48681	placental thrombin inhibitor - human	269	9.00e-72	MG	
			I38202	leupin precursor - human	267	3.00e-71	MG	
			XP_03695 1.4	similar to Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin)	266	8.00e-71	MG	
			15988197	Human Plasminogen Activator Inhibitor-2.[loop (66-98) Deletionmutant] Complexed With Peptide Mimicking The Reactive Center Loop	265	2.00e-70	MG	
			2118383	squamous cell carcinoma antigen 1	264	3.00e-70	MG	
NM_0083 41 NP_0323 67.1	Mm.213 00	F:(C-HI) -3.37, F:(C-D) -3.47, F:(HI-D) -2.63	AAH3526 3.1	Similar to insulin-like growth factor binding protein 1	384	1.00e-106	MG	
			CAA6877 0.1	IGF-binding preprotein (AA -25 to 234)	384	1.00e-106	MG	
			NP_00058 7.1	insulin-like growth factor binding protein 1	382	1.00e-106	MG	
			AAA5254 0.1	insulin-like growth factor binding protein 1	338	9.00e-93	MG	
			CAA3311 0.1	small IGF-binding-protein	198	5.00e-50	MG	
NM_0096 69 NP_0337 99.1	Mm.324	F:(C-HI) -3.13	NP_00069 0.1	amylase, alpha 2A; pancreatic; Amylase, pancreatic, alpha-2A	952	0	MG	
			NP_06618 8.1	amylase, alpha 2B; pancreatic; Amylase, pancreatic, alpha-2B	946	0	MG	
			XP_08698 8.1	similar to Alpha-amylase, salivary precursor (1,4-alpha-D-glucan glucanohydrolase)	941	0	MG	
			67366	alpha-amylase (EC 3.2.1.1) precursor, salivary - human	939	0	MG	

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			NP_004029.1	amylase, alpha 1A; salivary; Amylase, salivary, alpha-1A	939	0	MG	
			7245760	Chain A, Structure Of Human Pancreatic Alpha-Amylase In Complex With The Carbohydrate Inhibitor Acarbose	927	0	MG	
			1421331	Chain , Mol_id: 1; Molecule: Human Pancreatic Alpha-Amylase; Chain: Null; Ec: 3.2.1.1	925	0	MG	
			18655894	Chain A, Three Dimensional Structure Analysis Of The R195q Variant Of Human Pancreatic Alpha Amylase	924	0	MG	
			18655893	Chain A, Three Dimensional Structure Analysis Of The R337q Variant Of Human Pancreatic Alpha-Mylase	924	0	MG	
			14719496	Chain A, Subsite Mapping Of The Active Site Of Human Pancreatic Alpha-Amylase Using Substrates, The Pharmacological Inhibitor Acarbose, And An Active Site Variant	923	0	MG	
			20664071	Chain A, Mechanistic Analyses Of Catalysis In Human Pancreatic Alpha- Amylase: Detailed Kinetic And Structural Studies Of Mutants Of Three Conserved Carboxylic Acids	923	0	MG	
			20664068	Chain A, Three Dimensional Structure Analysis Of The R195a Variant Of Human Pancreatic Alpha Amylase	923	0	MG	
			18655892	Chain A, Three Dimensional Structure Analysis Of The R337a Variant Of Human Pancreatic Alpha-Amylase	923	0	MG	
			20664074	Chain A, Mechanistic Analyses Of Catalysis In Human Pancreatic Alpha- Amylase: Detailed Kinetic And Structural Studies Of Mutants Of Three Conserved Carboxylic Acids	922	0	MG	
			1633119	Chain , Human Salivary Amylase	919	0	MG	
			15988375	Chain A, Role Of Mobile Loop In The Mechanism Of Human Salivary Amylase	914	0	MG	
			15988376	Chain A, Role Of Ethe Mobile Loop In The Mehanism Of Human Salivary Amylase	904	0	MG	
			AAA57345.1	alpha-amylase	515	1.00e-146	MG	
U38940 AAA8512 5.1	Mm.294 2	F:(C-HI) -3.11, F:(C-D) -2.11	NP_001664.2	asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein	1035	0	MG	
			P08243	Asparagine synthetase [glutamine-hydrolyzing] (Glutamine-dependent asparagine synthetase) (TS11 cell cycle control protein)	1033	0	MG	
			AJHUN1	aspartate-ammonia ligase (EC 6.3.1.1) - human	1030	0	MG	
			XP_095404.4	similar to asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein	562	1.00e-160	MG	
J03953 AAA3774 8.1	Mm.371 99	F:(C-HI) -3.03	4388890	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	4.00e-97	MG	
			XP_002155.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1) .	352	4.00e-97	MG	
			AAA59203.1	glutathione transferase M1	350	2.00e-96	MG	



			4557966	Chain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	348	1.00e-95	MG	
			NP_00083 9.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	348	1.00e-95	MG	
			494185	Chain , Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	1.00e-94	MG	
			6980588	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	342	7.00e-94	MG	
5			NP_00084 1.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	342	7.00e-94	MG	
			AAA5734 6.1	glutathione transferase M4	340	2.00e-93	MG	
			S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2)	338	8.00e-93	MG	
			P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	337	1.00e-92	MG	
			NP_00084 2.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	336	3.00e-92	MG	
10			CAA4863 6.1	glutathione S-transferase	302	6.00e-82	MG	
			AAH1783 6.1	Similar to glutathione S-transferase M2 (muscle)	299	5.00e-81	MG	
			XP_04272 2.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	297	2.00e-80	MG	
			AAH0879 0.1	Unknown (protein for MGC:3704)	297	2.00e-80	MG	
			5822511	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	297	2.00e-80	MG	
15			NP_67148 9.1	hione S-transferase M4 Isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	296	3.00e-80	MG	
			A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3	284	2.00e-79	MG	
			XP_16702 3.1	similar to glutathione transferase M2	277	2.00e-74	MG	
			NP_66653 3.1	glutathione S-transferase M1 Isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	270	2.00e-72	MG	

5	NM_013459 NP_038487.1	Mm.4407	F:(C-HI) -2.94	P00746	Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)	370	1.00e-102	MG	
				CAC48304.1	adipsin/complement factor D precursor	358	4.00e-99	MG	
				67580	complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)	352	5.00e-97	MG	
				6730437	Chain A, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	340	1.00e-93	MG	
				1633237	Chain , Mutant Of Factor D With Enhanced Catalytic Activity	330	1.00e-90	MG	
				5542120	Chain , Human Complement Factor D In Complex With Isatoic Anhydride Inhibitor	329	3.00e-90	MG	
				XP_084037.1	similar to Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)	328	8.00e-90	MG	
				NP_001919.1	adipsin/complement factor D precursor	324	1.00e-88	MG	
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15	NM_016810 NP_058090.1	Mm.20931	F:(C-HI) -2.86	NP_004862.1	golgi SNAP receptor complex member 1; Golgi SNARE 28 kDa	477	1.00e-134	MG	
				AAC39889.1	GOS28/P28 protein	452	1.00e-127	MG	
				AAH12620.1	Similar to golgi SNAP receptor complex member 1	218	1.00e-56	MG	
20									
25	AK006128 BAB24422.1	Mm.23942	F:(C-HI) -2.71	AAD01430.1	MRP3	365	1.00e-101	MG	
				AAD38185.1	MRP3s1 protein	365	1.00e-101	MG	
				NP_003777.2	ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter	365	1.00e-101	MG	
30				CAA76658.2	multidrug resistance protein 3 (ABCC3)	365	1.00e-101	MG	
				BAA28146.1	multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2)	365	1.00e-101	MG	
				JE0336	canicular multispecific organic anion transporter	364	1.00e-100	MG	
				AAB71756.1	multidrug resistance-associated protein homolog	350	2.00e-96	MG	
				CAC69553.1	multidrug resistance associated protein	331	1.00e-90	MG	
				AAH01636.1	Unknown (protein for IMAGE:3355848)	313	3.00e-85	MG	
				NP_063954.1	ATP-binding cassette, sub-family C, member 1, isoform 4; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85	MG	
				AAB83979.1	multidrug resistance protein	313	3.00e-85	MG	
				NP_063953.1	ATP-binding cassette, sub-family C, member 1, isoform 3; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85	MG	

			NP_00498 7.1	ATP-binding cassette, sub-family C, member 1, isoform 1; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e- 85	MG	
			DVHUAR	multidrug resistance protein (cell line H69AR)	313	3.00e- 85	MG	
			NP_06391 5.1	ATP-binding cassette, sub-family C, member 1, isoform 2; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e- 85	MG	
			NP_06395 7.1	ATP-binding cassette, sub-family C, member 1, isoform 7; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e- 85	MG	
5			AAC1578 4.1	Multiple drug resistance gene MRP1 (5' partial)	313	3.00e- 85	MG	
			AAB8398 2.1	multidrug resistance protein	313	3.00e- 85	MG	
			AAB8398 0.1	multidrug resistance protein	313	3.00e- 85	MG	
			NP_06395 6.1	ATP-binding cassette, sub-family C, member 1, isoform 6; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e- 85	MG	
			AAB8398 1.1	multidrug resistance protein	313	3.00e- 85	MG	
10			AAB0942 2.1	canalicular multispecific organic anion transporter	279	5.00e- 75	MG	
			NP_00038 3.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 2; canalicular multispecific organic anion transporter	277	2.00e- 74	MG	
			S71841	multidrug resistance protein, canalicular	276	3.00e- 74	MG	
			CAB4530 9.1	multidrug resistance protein 2 (MRP2)	276	3.00e- 74	MG	
15	NM_0087 42 NP_0327 68.1	Mm.200 703 F:(C-HI) -2.68	NP_00251 8.1	neurotrophin 3 precursor	449	1.00e- 141	MG	
			5542321	Chain A, Human Neurotrophin-3	255	5.00e- 68	MG	
			1421251	Chain B, Neurotrophin Mol_id: 1; Molecule: Brain Derived Neurotrophic Factor; Chain: A; Synonym: Bdnf; Engineered: Yes; Mol_id: 2; Molecule: Neurotrophin 3; Chain: B; Synonym: Nt3; Engineered: Yes; Other_details: Heterodimer	249	4.00e- 68	MG	
20	NM_0083 61 NP_0323 87.1	Mm.221 50 F:(C-HI) -2.65, F:(C-D) -2.03	NP_00056 7.1	interleukin 1, beta	352	3.00e- 97	MG	
			P01584	Interleukin-1 beta precursor (IL-1 beta) (Catabolin)	350	1.00e- 96	MG	
25			AAA5913 6.1	interleukin 1	345	6.00e- 95	MG	
			AAC0353 6.1	interleukin 1 beta	240	2.00e- 63	MG	
			1827779	Chain , Interleukin-1 Beta From Joint X-Ray And Nmr Refinement	239	2.00e- 63	MG	

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			230947	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 8 Replaced By Ala (C8A)	239	3.00e-63	MG	
			494152	Chain , Interleukin-1 Beta (Human) Mutant With Thr 9 Replaced By Gly (T8g)	239	3.00e-63	MG	
			230410	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 71 Replaced By Ala) (C71A)	236	3.00e-62	MG	
			230798	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 71 Replaced By Ser) (C71S)	236	4.00e-62	MG	
AF294617 AAG02118.1	Mm.19669	F:(C-HI) -2.63	NP_004557.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase	1030	0	MG	
			AAB99795.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	1028	0	MG	
			JC4626	6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46)	1028	0	MG	
			AAC62000.1	Inducible 6-phosphofructo-2-kinase/fructose 2,6-bisphosphatase	1005	0	MG	
			CAA06605.1	6-phosphofructo-2-kinase	699	0	MG	
			O60825	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 (6PF-2-K/Fru-2,6-P2ASE heart-type isozyme) (PFK-2/FBPase-2) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase ]	697	0	MG	
			NP_006203.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; Fructose-2,6-bisphosphatase, cardiac isozyme	688	0	MG	
			BAB19681.1	6-phosphofructo-2-kinase heart isoform	680	0	MG	
			NP_004558.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	670	0	MG	
			JC5871	6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46)	669	0	MG	
			NP_002616.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1; Fructose-2,6-bisphosphatase	668	0	MG	
			P16118	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase ]	668	0	MG	
			CAB06077.1	6-phosphofructo-2-kinase	589	1.00e-167	MG	
NM_009998 NP_034128.1	Mm.14177	F:(C-HI) -2.61, F:(C-D) -2.33	NP_000758.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	701	0	MG	
			AAF13602.1	cytochrome P450-2B6	692	0	MG	
			AAA52143.1	cytochrome P450-IIB	511	1.00e-144	MG	
NM_008988 NP_033014.1	Mm.10689	F:(C-HI) -2.6	XP_116965.2	similar to punc	695	0	MG	
			NP_066013.1	DDM36	390	1.00e-108	MG	

			AAD1339 9.1	putative neuronal cell adhesion molecule	384	1.00e-106	MG	
			AAA3575 1.1	colorectal tumor suppressor (put.); putative	254	7.00e-67	MG	
			NP_00520 6.1	deleted in colorectal carcinoma	254	7.00e-67	MG	
5	NM_010166 NP_034296.1	Mm.1430 F:(C-HI) -2.57	Q99504	Eyes absent homolog 3	778	0	MG	
			CAA7131 1.1	EYA3	763	0	MG	
10			NP_00198 1.1	eyes absent homolog 3 (Drosophila);	644	0	MG	
			AAH1419 3.1	Unknown (protein for IMAGE:4110403)	438	1.00e-122	MG	
			NP_00409 1.1	eyes absent homolog 4 (Drosophila);	436	1.00e-122	MG	
			NP_00049 4.2	eyes absent 1 isoform b; Eyes absent, Drosophila, homolog of, 1; Melnick-Fraser syndrome	431	1.00e-120	MG	
			CAA7130 9.1	EYA1A	431	1.00e-120	MG	
15			AAH0880 3.1	Similar to eyes absent (Drosophila) homolog 2	399	1.00e-110	MG	
			AAH0028 9.1	Similar to eyes absent (Drosophila) homolog 2	394	1.00e-109	MG	
			O00167	Eyes absent homolog 2	394	1.00e-109	MG	
			AAC0936 2.1	eyes absent homolog	394	1.00e-109	MG	
			NP_00523 5.2	eyes absent homolog 2	392	1.00e-108	MG	
20			AAL7343 7.1	EYA1D	380	1.00e-104	MG	
			AAB4206 5.1	EYA2 homolog	318	3.00e-86	MG	
25	AK002480 NP_666065.1	Mm.28301 F:(C-HI) -2.55, F:(C-D) -2.57	NP_00189 3.2	cystathionase isoform 1; cystathionine gamma-lyase; homoserine deaminase; homoserine dehydratase; cysteine desulfhydrase	574	1.00e-163	MG	
			P32929	Cystathionine gamma-lyase	574	1.00e-163	MG	
			CAC1290 1.1	bA42O15.1.2 (cystathionase (cystathionine gamma-lyase))	480	1.00e-135	MG	
			JC1362	cystathionine gamma-lyase (EC 4.4.1.1)	480	1.00e-135	MG	
30	AK018226 XP_110043.1	Mm.92685 F:(C-HI) -2.53, F:(C-D) -2.4	NP_10959 1.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	345	1.00e-138	MG	
			NP_00414 6.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)	200	5.00e-79	MG	
			NP_00263 1.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	207	2.00e-76	MG	

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			NP_00501 5.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)	179	4.00e-75	MG	
			NP_00455 9.2	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	192	4.00e-75	MG	
			I5988197	Chain A, Human Plasminogen Activator Inhibitor-2 [loop (66-98) Deletionmutant] Complexed With Peptide Mimicking The Reactive Center Loop	199	5.00e-75	MG	
			S39661	placental thrombin inhibitor - human	190	3.00e-74	MG	
NM_0103 61 NP_0344 91.1	Mm.241 18	F:(C-HI) -2.46, F:(C-D) -2.25	NP_00084 5.1	glutathione S-transferase theta 2	375	1.00e-104	MG	
			AAG0237 3.1	glutathione S-transferase theta 2	375	1.00e-104	MG	
			AAC1331 7.1	glutathione S-transferase theta 2	364	1.00e-101	MG	
			XP_05601 6.1	similar to Glutathione S-transferase theta 1 (GST class-theta) (Glutathione transferase T1-1)	239	3.00e-63	MG	
			NP_00084 4.1	glutathione S-transferase theta 1	239	4.00e-63	MG	
			AAH0706 5.1	glutathione S-transferase theta 1	236	2.00e-62	MG	
AK01848 5 BAB3123 3.1	Mm.233 36	F:(C-HI) -2.46	XP_06438 3.2	similar to data source:SPTR, source key:Q60928, evidence:ISS~putative~similar to GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE) (GGT)	261	1.00e-105	MG	
			NP_69916 9.1	hypothetical protein FLJ90165	211	5.00e-90	MG	
NM_0109 24 NP_0350 54.1	Mm.836 2	F:(C-HI) -2.45, F:(C-D) -2.19	NP_00616 0.1	nicotinamide N-methyltransferase	458	1.00e-129	MG	
			AAD0472 3.1	thioether S-methyltransferase-like; similar to P40936 (PID:g731019)	268	1.00e-71	MG	
			O95050	Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)	266	3.00e-71	MG	
			NP_00676 5.3	indolethylamine N-methyltransferase; thioester S-methyltransferase-like	265	6.00e-71	MG	
			AAH3381 3.1	Unknown (protein for IMAGE:5209218)	263	2.00e-70	MG	
NM_0213 07 NP_0672 82.1	Mm.826 78	F:(C-HI) -2.44	AAG2396 8.1	ZNF228 protein	107 8	0	MG	
			XP_00936 3.3	similar to ZNF228 protein	107 8	0	MG	
			NP_03751 2.1	zinc finger protein 228	107 3	0	MG	
			NP_05752 8.1	zinc finger protein 226; Kruppel-associated box protein	621	1.00e-177	MG	

			Q9NYT6	Zinc finger protein 226	621	1.00e-177	MG	
			AAF8810 3.1	zinc finger protein 226	619	1.00e-176	MG	
			NP_00422 5.2	zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)	579	1.00e-185	MG	
			AAF8810 7.1	Hypothetical zinc finger-like protein	579	1.00e-164	MG	
5			XP_09190 6.2	similar to Zinc finger protein 229	550	1.00e-156	MG	
			AAF7687 5.1	zinc finger protein	539	1.00e-152	MG	
			NP_00341 6.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain	533	1.00e-151	MG	
			AAF6303 0.1	Zinc finger protein ZNF45	530	1.00e-150	MG	
10	NM_0082 95 NP_0323 21.1	Mm.179 10 F:(C-HI) -2.43, F:(C-D) -5.64, F:(HI-D) -2.32	NP_00085 3.1	hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid delta-isomerase 1; Hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid	528	1.00e-149	MG	
			AAA5183 1.1	3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4-isomerase	526	1.00e-149	MG	
			NP_00018 9.1	hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid delta-isomerase 2; Hydroxy-delta-5-steroid dehydrogenase, 3 beta-and steroid	513	1.00e-145	MG	
15			AAA3600 1.1	3-beta-hydroxysteroid dehydrogenase gene	481	1.00e-136	MG	
			CAC1980 1.1	dJ871G17.4 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	360	3.00e-99	MG	
			AAM0870 4.1	3-beta-hydroxysteroid dehydrogenase	353	5.00e-97	MG	
			XP_06082 1.1	similar to dJ871G17.4 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	335	1.00e-91	MG	
			XP_06082 7.5	similar to 3-beta-hydroxysteroid dehydrogenase	258	2.00e-68	MG	
20			XP_08933 4.1	similar to 3 BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5->4-ISOMERASE (3BETA-HSD)	238	1.00e-62	MG	
			AAG3782 4.1	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	225	2.00e-58	MG	
			NP_07946 9.2	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	223	8.00e-58	MG	
			XP_06082 2.5	similar to dJ871G17.6 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member )	213	6.00e-55	MG	
			CAC1980 3.1	dJ871G17.8 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member )	202	8.00e-52	MG	
25			AAD1441 4.1	3 beta-hydroxysteroid dehydrogenase homolog pseudogene	199	7.00e-51	MG	

NM_010001 NP_034131.1	Mm.38963	F:(C-HI) -2.43, F:(C-D) -2.56	NP_000763.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	669	0	MG
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	667	0	MG
			NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	653	0	MG
			BAA00123.1	cytochrome P-450	650	0	MG
			NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	650	0	MG
			AAB23864.2	cytochrome P-450	650	0	MG
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-)	848	0	MG
			I506290A	cytochrome P450 2C19 - human	646	0	MG
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	645	0	MG
			AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	645	0	MG
			I52418	cytochrome P450 - human	629	1.00e-180	MG
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	624	1.00e-178	MG
AK012213 BAB28101.1	Mm.24457	F:(C-HI) -2.39, F:(C-D) -2.05	A40872	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 5 precursor, mitochondrial	948	0	MG
			CAD13246.1	ba113024.2 (aldehyde dehydrogenase 1 family, member B1 (ALDH5 ALDHX))	948	0	MG
			NP_000683.2	aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5	947	0	MG
			P30837	Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)	944	0	MG
			XP_007012.1	similar to Aldehyde dehydrogenase, mitochondrial precursor (ALDH class 2) (ALDH1) (ALDH-E2)	756	0	MG
			6137677	Chain A, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	756	0	MG
			AAA51693.1	aldehyde dehydrogenase	755	0	MG
			NP_000681.1	aldehyde dehydrogenase 2 family (mitochondrial); aldehyde dehydrogenase 2, mitochondrial	741	0	MG
			CAA68290.1	precursor polypeptide (AA -36 to 479)	738	0	MG
			O94788	Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	684	0	MG
			NP_003879.1	aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2	684	0	MG



			AAC5165 2.1	aldehyde dehydrogenase 1	655	0	MG	
			NP_00068 0.2	aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1	655	0	MG	
			NP_00068 4.1	aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6	650	0	MG	
			AAB5950 0.1	aldehyde dehydrogenase 2 (EC 1.2.1.3)	604	1.00e-172	MG	
5			AAH3058 9.1	Similar to aldehyde dehydrogenase 1 family, member A2	599	1.00e-171	MG	
			BAA3478 6.1	RALDH2-T	598	1.00e-170	MG	
			I39431	aldehyde dehydrogenase I - human (fragment).	467	1.00e-131	MG	
			NP_03632 2.2	formyltetrahydrofolate dehydrogenase isoform a	438	1.00e-122	MG	
			XP_09029 4.1	similar to 10-formyltetrahydrofolate dehydrogenase	434	1.00e-121	MG	
10			O75891	10-formyltetrahydrofolate dehydrogenase (10-FTHFDH)	433	1.00e-121	MG	
	NM_0231 54 NP_0756 43.1	Mm.295 53 F:(C-HI) -2.39, F:(C-D) -2.48	AAH0825 0.1	Similar to RIKEN cDNA 0610025L15 gene	456	1.00e-128	MG	
15			AAG0906 3.1	protein expressed in thyroid	437	1.00e-123	MG	
			NP_05511 2.1	protein expressed in thyroid	434	1.00e-122	MG	
	NM_0104 01 NP_0345 31.1	Mm.130 00 F:(C-HI) -2.39, F:(C-D) -2.21	BAB6186 3.1	histidase	121	6	0	MG
20			NP_00209 9.1	histidine ammonia-lyase; Histidine ammonia-lyase (histidase)	121	5	0	MG
	NM_0234 55 NP_0759 44.1	Mm.154 782 F:(C-HI) -2.39, F:(C-D) -2.04	NP_05743 1.1	putative N-acetyltransferase Camello 2	223	4.00e-58	MG	
25			NP_00395 1.2	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene	216	3.00e-56	MG	
			BAA7164 3.1	GLA	216	4.00e-56	MG	
			AAH1262 6.1	kidney- and liver-specific gene	214	1.00e-55	MG	
			T44342	hypothetical protein TSC501	214	1.00e-55	MG	
30	NM_0187 79 NP_0612 49.1	Mm.103 728 F:(C-HI) -2.35, F:(C-D) -2.43	CAA0630 4.1	phosphodiesterase 3A	137	9	0	MG
			Q14432	cGMP-inhibited 3',5'-cyclic phosphodiesterase A (Cyclic GMP inhibited phosphodiesterase A) (CGI-PDE A)	137	9	0	MG
35			NP_00091 2.2	phosphodiesterase 3A, cGMP-inhibited	137	9	0	MG

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			A44093	cGMP-inhibited cAMP phosphodiesterase (EC 3.1.4.-), myocardial form - human	1378	0	MG	
			CAA6477 4.1	cyclic nucleotide phosphodiesterase	677	0	MG	
			NP_00091 3.1	phosphodiesterase 3B, cGMP-inhibited	677	0	MG	
	AK00956 3	Mm.286 97	F:(C-HI) -2.33	XP_04558 5.1	similar to RIKEN cDNA 2310032D16	929	0	MG
	BAB2636 1.1			BAA9267 2.1	KIAA1434 protein	929	0	MG
				BAA9199 4.1	unnamed protein product	444	1.00e-124	MG
	NM_0094 66	Mm.107 09	F:(C-HI) -2.32,	NP_00335 0.1	UDP-glucose dehydrogenase	971	0	MG
	NP_0334 92.1		F:(C-D) -2.00	JE0353	uridine diphosphoglucose dehydrogenase (EC 1.-.-.-)	958	0	MG
				AAC0513 5.1	UDP glucose 6-dehydrogenase	337	4.00e-92	MG
				CAB9817 9.1	uridine diphospho-glucose dehydrogenase	320	7.00e-87	MG
				CAB9817 8.1	uridine diphospho-glucose dehydrogenase	288	2.00e-77	MG
	NM_0135 84	Mm.317 4	F:(C-HI) -2.31,	NP_00230 1.1	leukemia inhibitory factor receptor precursor	1663	0	MG
	NP_0386 12.1		F:(C-D) -2.46	AAB2388 4.1	leukaemia inhibitory factor receptor, LIF receptor [human, placenta, Peptide, 1078 aa]	1640	0	MG
				NP_00399 0.1	oncostatin M receptor	345	2.00e-94	MG
				AAB6189 7.1	leukemia inhibitory factor receptor	282	2.00e-75	MG
	NM_0080 61	Mm.180 64	F:(C-HI) -2.28,	NP_00014 2.1	glucose-6-phosphatase, catalytic	588	1.00e-168	MG
	NP_0320 87.1		F:(C-D) -2.14	AAH2070 0.1	Unknown (protein for MGC:22459)	416	1.00e-115	MG
				NP_06699 9.1	islet-specific glucose-6-phosphatase catalytic subunit-related p	318	2.00e-86	MG
	NM_0256 31	Mm.464 48	F:(C-HI) -2.25,	NP_07950 3.1	hypothetical protein dJ726C3.2 [	558	1.00e-159	MG
	NP_0799 07.1		F:(C-D) -2.16	AAH3441 5.1	hypothetical protein dJ726C3.2	555	1.00e-158	MG
	NM_0254 04	Mm.537 6	F:(C-HI) -2.24,	AAH0004 3.1	ADP-ribosylation factor 4-like	359	6.00e-99	MG
	NP_0796 80.1		F:(C-D) -2.03	NP_00165 2.1	ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6	357	2.00e-98	MG
				AAA9322 9.1	ADP-ribosylation factor	348	1.00e-95	MG

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			XP_04589 0.2	similar to ADP-ribosylation factor 4L	245	4.00e-70	MG	
			NP_00572 9.1	ADP-ribosylation factor-like 4	233	4.00e-61	MG	
			NP_00572 8.2	ADP-ribosylation factor-like 7	222	8.00e-58	MG	
			XP_16670 3.1	similar to ADP-ribosylation-like 4	213	5.00e-55	MG	
			BAA7547 3.1	ADP ribosylation factor-like protein	209	1.00e-53	MG	
NM_0086 15 NP_0326 41.1	Mm.148 155	F:(C-HI) -2.22	JC4160	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40)	101 3	0	MG	
			AAB0138 0.1	NADP-dependent malic enzyme	101 3	0	MG	
			NP_00238 6.1	cytosolic malic enzyme 1; malic enzyme, cytoplasmic; malic enzyme 1, soluble; NADP-dependent malic enzyme; malate dehydrogenase; pyruvic-malic carboxylase	977	0	MG	
			AAC5061 3.1	cytosolic NADP(+)-dependent malic enzyme	974	0	MG	
			NP_00667 1.1	malic enzyme 3, NADP(+)-dependent, mitochondrial; malic enzyme, NADP+-dependent, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase; NADP-ME	799	0	MG	
			AAH2247 2.1	malic enzyme 3, NADP(+)-dependent, mitochondrial	796	0	MG	
			NP_00238 7.1	malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochondrial; malic enzyme 2, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase	624	1.00e-178	MG	
NM_0261 04 NP_0803 80.1	Mm.148 837	F:(C-HI) -2.22	XP_08528 1.2	similar to RIKEN cDNA 1700095F04	305	1.00e-82	MG	
			BAC0406 5.1	unnamed protein product	229	4.00e-60	MG	
NM_0087 92 NP_0328 18.1	Mm.124 7	F:(C-HI) -2.19	NP_00258 5.2	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5	124 7	0	MG	
			AAA6003 2.1	endoprotease	124 4	0	MG	
			CAB8942 8.1	dJ531H18.1 (proprotein convertase subtilisin/kexin type 2 (NEC2))	892	0	MG	
			NP_00043 0.3	proprotein convertase subtilisin/kexin type 1 preproprotein; prohormone convertase 3; prohormone convertase 1; neuroendocrine convertase 1; proprotein convertase 1	509	e-144	MG	
NM_0137 43 NP_0387 71.1	Mm.102 83	F:(C-HI) -2.19	NP_00260 3.1	pyruvate dehydrogenase kinase, isoenzyme 4	764	0	MG	
			NP_00260 1.1	pyruvate dehydrogenase kinase, isoenzyme 1	562	1.00e-159	MG	
			NP_00260 2.2	pyruvate dehydrogenase kinase, isoenzyme 2	558	1.00e-158	MG	

			I70159	pyruvate dehydrogenase (lipoamide) kinase (EC 2.7.1.99) 2	554	1.00e-157	MG	
			NP_00538 2.1	pyruvate dehydrogenase kinase, isoenzyme 3	527	1.00e-149	MG	
5	NM_0103 57 NP_0344 87.1	Mm.266 2 F:(C-HI) -2.17, F:(C-D) -2.93	Q16772	Glutathione S-transferase A3-3 (GST class-alpha)	264	1.00e-70	MG	
			NP_00083 8.2	glutathione S-transferase A3	263	3.00e-70	MG	
			A49365	glutathione transferase (EC 2.5.1.18) alpha-3 [similarity]	261	1.00e-69	MG	
			NP_66568 3.1	glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2	261	1.00e-69	MG	
10			AAA7463 4.1	glutathione S-transferase A3	261	1.00e-69	MG	
			S27110	glutathione transferase (EC 2.5.1.18) A2	259	3.00e-69	MG	
			S24330	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human	259	4.00e-69	MG	
			CAB9277 0.1	dJ152L7.3 (glutathione S-transferase A2)	259	5.00e-69	MG	
			442977	Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)	259	5.00e-69	MG	
15			NP_00083 7.2	glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-alkyltransferase A2; GST-gamma; HA subunit 2	258	6.00e-69	MG	
			I127144	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k)	258	2.00e-68	MG	
			S20331	glutathione transferase (EC 2.5.1.18)	256	2.00e-68	MG	
			DAA0007 1.1	TPA: glutathione transferase A5	256	3.00e-68	MG	
			I52381	glutathione transferase (EC 2.5.1.18)	254	9.00e-68	MG	
20			XP_16710 0.2	similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha)	253	3.00e-67	MG	
			A56801	glutathione transferase (EC 2.5.1.18) alpha y	252	5.00e-67	MG	
			S77958	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2 (+)) - human	248	7.00e-66	MG	
			NP_00150 3.1	glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-alkyltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4	244	1.00e-64	MG	
25	NM_0111 46 NP_0352 76.1	Mm.302 0 F:(C-HI) -2.17	NP_05695 3.2	peroxisome proliferative activated receptor gamma, isoform 2; PPAR-gamma; peroxisome proliferator activated receptor gamma	953	0	MG	

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			BAA1894 9.1	PPAR gamma2	939	0	MG	
			S42489	peroxisome proliferator activated receptor - human	922	0	MG	
			CAA6215 2.1	peroxisome proliferator activated receptor gamma	916	0	MG	
			NP_00502 8.3	peroxisome proliferative activated receptor gamma, isoform 1; PPAR-gamma; peroxisome proliferator activated receptor gamma	914	0	MG	
			BAA2335 4.1	ome proliferator activated-receptor gamma	904	0	MG	
			20150106	Chain A, Crystal Structure Of The Ligand Binding Domain Of Human Ppar-Gamma In Complex With The Agonist Az 242	511	1.00e-144	MG	
NM_0073 95 NP_0314 21.1	Mm.507 0	F:(C-HI) -2.16	NP_00429 3.1	activin A type IB receptor precursor; serine(threonine) protein kinase	931	0	MG	
			NP_06473 2.1	activin A type IB receptor, isoform b precursor; serine(threonine) protein kinase	849	0	MG	
			I80182	activin type I receptor SKR2, splice form 2	842	0	MG	
			NP_06473 3.1	activin A type IB receptor, isoform c precursor; serine(threonine) protein kinase	756	0	MG	
			I80183	activin type I receptor SKR2 splice form 3	749	0	MG	
			NP_00460 3.1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa); transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kD)	641	0	MG	
			XP_06571 2.3	similar to activin receptor-like kinase 7	593	1.00e-169	MG	
			NP_66030 2.1	activin receptor-like kinase 7	590	1.00e-168	MG	
			I5988007	Chain A, Cytoplasmic Domain Of Unphosphorylated Type I Tgf-Beta Receptor Crystallized Without Fkbp12	573	1.00e-163	MG	
			NP_00119 4.1	bone morphogenetic protein receptor, type IB; serine/threonine receptor kinase	417	1.00e-116	MG	
			AAH2838 3.1	e morphogenetic protein receptor, type IA	413	1.00e-115	MG	
			NP_00432 0.1	bone morphogenetic protein receptor, type IA precursor; activin A receptor, type II-like kinase 3	413	1.00e-115	MG	
			I80180	activin type I receptor SKR2-1	404	1.00e-112	MG	
			NP_00109 6.1	activin A type I receptor precursor; hydroxyalkyl-protein kinase; activin A receptor, type II-like kinase 2	399	1.00e-111	MG	
			P37023	Serine/threonine-protein kinase receptor R3 precursor (SKR3) (Activin receptor-like kinase 1) (ALK-1) (TGF-B superfamily receptor type I) (TSR-I)	369	1.00e-102	MG	
			NP_00001 1.1	activin A receptor type II-like 1; Activin A receptor, type II-like kinase 1	369	1e-1-1	MG	
			I59318	activin type I receptor SKR2-2	325	2.00e-88	MG	
			I80181	activin type I receptor SKR2-3 - human	232	1.00e-60	MG	
			A42100	transforming growth factor beta receptor type IIB precursor	206	1.00e-52	MG	

5	NM_009127 NP_033153.1	Mm.140785	F:(C-HI) -2.15, F:(C-D) -3.29, F:(HI-D) -2.71	NP_005054.2	stearoyl-CoA desaturase (delta-9-desaturase)	597	1.00e-170	MG	
				O00767	Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)	596	1.00e-170	MG	
				AAH05807.1	Unknown (protein for MGC:10264)	592	1.00e-169	MG	
				CAA73998.1	stearoyl CoA desaturase	589	1.00e-168	MG	
				AAF71040.1	PRO0998	579	1.00e-165	MG	
				AAH06288.1	Unknown (protein for MGC:10270)	422	1.00e-118	MG	
				I54779	stearoyl-CoA desaturase - human (fragment)	377	1.00e-104	MG	
				CAD38567.1	hypothetical protein	216	6.00e-56	MG	
15	NM_007824 NP_031850.1	Mm.57029	F:(C-HI) -2.14, F:(C-D) -3.09	P22680	Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase)	865	0	MG	
				NP_000771.1	cytochrome P450, subfamily VIIA, polypeptide 1; cholesterol 7-alpha-hydroxylase; cholesterol 7 alpha-monooxygenase	861	0	MG	
				AAC95426.1	oxysterol 7alpha-hydroxylase	342	8.00e-94	MG	
				NP_004811.1	cytochrome P450, subfamily VIIB, polypeptide 1; oxysterol 7alpha-hydroxylase	342	8.00e-94	MG	
				NP_004382.1	cytochrome P450, subfamily VIIB, polypeptide 1; 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-hydroxylase CYP8B1	298	2.00e-80	MG	
				AAC63037.1	sterol 12-alpha hydroxylase CYP8B1	279	7.00e-75	MG	
				AAA61350.1	CYP7	259	9.00e-69	MG	
20									
25	AK002979 BAB22492.1	Mm.195881	F:(C-HI) -2.14, F:(C-D) -2.15	NP_056537.1	calcyon	336	5.00e-92	MG	
30	NM_011817 NP_035947.1	Mm.9653	F:(C-HI) -2.13	BAA84543.1	gadd45-related protein	313	2.00e-85	MG	
				NP_006696.1	growth arrest and DNA-damage-inducible, gamma; GADD45-gamma; gadd-related protein, 17 kD	307	2.00e-83	MG	
				AAK00414.1	growth arrest and DNA damage inducible protein gamma	303	3.00e-82	MG	
35	NM_027000 NP_081276.1	Mm.41800	F:(C-HI) -2.13	XP_040267.1	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB)	996	0	MG	
				BAA91752	unnamed protein product	994	0	MG	

			NP_03647 3.1	G protein-binding protein CRFG; GTP-binding protein	991	0	MG	
			AAH3378 4.1	G protein-binding protein CRFG	982	0	MG	
			AAC2436 4.1	putative G-binding protein	828	0	MG	
5	NM_0078 15 NP_0318 41.1	Mm.207 64 F:(C-HI) -2.11, F:(C-D) -2.78	NP_00076 3.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	725	0	MG	
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	723	0	MG	
10			NP_00076 0.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	711	0	MG	
			AAB2386 4.2	cytochrome P-450	710	0	MG	
			BAA0012 3.1	cytochrome P-450	710	0	MG	
			NP_00076 2.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	710	0	MG	
			I506290A	cytochrome P450	706	0	MG	
15			AAA5215 7.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	706	0	MG	
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-B) (S-mephenytoin 4-hydroxylase) (P-450MP)	706	0	MG	
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	705	0	MG	
			I52418	cytochrome P450 - human	676	0	MG	
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	668	0	MG	
20			AAH2059 6.1	Unknown (protein for MGC:22146)	667	0	MG	
			NP_00076 1.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	665	0	MG	
			AAA5216 0.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	664	0	MG	
			S66382	cytochrome P450 2C8 - human	664	0	MG	
			AAB3529 2.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	664	0	MG	
25			AAA5216 1.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	660	0	MG	
			AAA5215 9.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	598	1.00e-170	MG	

AK00648 7 BAB2461 2.1	Mm.271 96	F:(C-HI) -2.1	NP_62013 4.1	hypothetical protein BC015148	445	1.00e- 125	MG
NM_0085 87 NP_0326 13.1	Mm.458 2	F:(C-HI) -2.1	AAG3312 9.1	MER receptor tyrosine kinase	155 0	0	MG
			NP_00633 4.1	c-met proto-oncogene tyrosine kinase	154 8	0	MG
			B41527	transforming protein (axl(-)) - human	620	1.00e- 177	MG
			NP_00169 0.2	AXL receptor tyrosine kinase isoform 2; AXL transforming sequence/gene; oncogene AXL	619	1.00e- 177	MG
			AAH3222 9.1	Unknown (protein for MGC:34202)	619	1.00e- 177	MG
			NP_06871 3.2	AXL receptor tyrosine kinase isoform 1; AXL transforming sequence/gene; oncogene AXL	619	1.00e- 177	MG
			P30530	Tyrosine-protein kinase receptor UFO precursor (AXL oncogene)	619	1.00e- 177	MG
			CAA4033 8.1	unnamed protein product	619	1.00e- 176	MG
			Q06418	Tyrosine-protein kinase receptor TYRO3 precursor (Tyrosine-protein kinase RSE) (Tyrosine-protein kinase SKY) (Tyrosine-protein kinase DTK) (Protein-tyrosine kinase byk)	601	1.00e- 171	MG
			NP_00628 4.1	TYRO3 protein tyrosine kinase; Brl; Dtk; Sky; Tif; Tyro3 protein tyrosine kinase (sea-related receptor tyrosine kinase)	600	1.00e- 171	MG
			BAA2178 1.1	protein-tyrosine kinase	595	1.00e- 169	MG
			I38412	receptor tyrosine kinase - human	602	1.00e- 141	MG
			A56379	ZP3 receptor precursor - human	415	1.00e- 118	MG
			AAH2992 5.1	Similar to TYRO3 protein tyrosine kinase	417	1.00e- 116	MG
			CAA5139 6.1	TYRO3	384	1.00e- 100	MG
NM_0079 12 NP_0319 38.1	Mm.853 4	F:(C-HI) -2.09, F:(C-D) -2.69	P00533	Epidermal growth factor receptor precursor (Receptor protein-tyrosine kinase ErbB-1)	116 0	0	MG
			AAA5237 1.1	aberrant epidermal growth factor receptor	116 0	0	MG
			NP_00521 9.1	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian); epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Epidermal growth factor receptor	115 7	0	MG
			AAG3578 6.1	p110 epidermal growth factor receptor	114 1	0	MG
			AAG3579 0.1	truncated epidermal growth factor receptor	114 1	0	MG
			CAA2528 2.1	EGF (1 is 2nd base in codon)	942	0	MG
			1007208A	epidermal growth factor receptor	884	0	MG
			AAC5080 2.1	epidermal growth factor receptor precursor	700	0	MG



			NP_00522 6.1	v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4	626	1.00e-179	MG	
			NP_00197 3.1	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian); Transformation gene ERBB-3; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	603	1.00e-172	MG	
			A36223	kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human	602	1.00e-172	MG	
			P21860	Receptor protein-tyrosine kinase erbB-3 precursor (c-erbB3) (Tyrosine kinase-type cell surface receptor HER3)	602	1.00e-172	MG	
			22219397	Chain A, Structure Of The Her3 (ErbB3) Extracellular Domain	602	1.00e-172	MG	
			P04626	Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell surface receptor HER2) (MLN 19)	569	1.00e-162	MG	
			NP_00443 9.1	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog; Avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 2; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)	569	1.00e-162	MG	
			AAH0270 6.1	Similar to v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	292	2.00e-78	MG	
			AAD5600 9.2	herstatin	283	9.00e-76	MG	
NM_0101 45 NP_0342 75.1	Mm.907 5	F:(C-HI) -2.09, F:(C-D) -2.09	AAC4169 4.1	microsomal epoxide hydrolase	818	0	MG	
			NP_00011 1.1	epoxide hydrolase 1, microsomal (xenobiotic); Epoxide hydroxylase 1, microsomal (xenobiotic)	818	0	MG	
			AAA5238 9.1	epoxide hydrolase	816	0	MG	
			CAA6848 6.1	precursor polypeptide (AA -20 to 435)	811	0	MG	
			AAA5958 0.1	microsomal epoxide hydrolase (EC 3.3.2.3)	585	1.00e-167	MG	
NM_0096 76 NP_0338 06.1	Mm.267 87	F:(C-HI) -2.08	BAB4030 5.1	aldehyde oxidase	220 4	0	MG	
			Q06278	Aldehyde oxidase	217 4	0	MG	
			NP_00115 0.2	aldehyde oxidase 1	217 1	0	MG	
			P47989	Xanthine dehydrogenase/oxidase [Includes: Xanthine dehydrogenase (XD); Xanthine oxidase (XO) (Xanthine oxidoreductase)]	126 2	0	MG	
			AAA7528 7.1	xanthine dehydrogenase	126 1	0	MG	
			NP_00037 0.1	xanthine dehydrogenase; xanthine oxidase; xanthine dehydrogenase	125 5	0	MG	
			XP_00247 2.7	similar to Xanthine dehydrogenase/oxidase	915	0	MG	

			XP_17206 0.1	similar to ALDEHYDE OXIDASE HOMOLOG-1~data source:SPTR, source key:Q9ESH4, evidence:ISS~putative	838	0	MG	
5	NM_0100 12 NP_0341 42.1	Mm.208 89 F:(C-HI) -2.08	NP_00438 2.1	cytochrome P450, subfamily VIII B, polypeptide 1; 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-hydroxylase	711	0	MG	
			AAC6303 7.1	sterol 12-alpha hydroxylase CYP8B1	679	0	MG	
			AAG3178 4.1	prostacyclin synthase	334	2.00e- 91	MG	
			BAA2821 9.1	prostacyclin synthase	332	9.00e- 91	MG	
			NP_00095 2.1	prostaglandin I2 (prostacyclin) synthase	332	9.00e- 91	MG	
10			BAA1191 0.1	prostacyclin synthase	332	9.00e- 91	MG	
			AAG3178 5.1	prostacyclin synthase	330	4.00e- 90	MG	
			AAG3178 3.1	prostacyclin synthase	328	1.00e- 89	MG	
15	NM_0119 21 NP_0360 51.1	Mm.146 09 F:(C-HI) -2.08	AAC5165 2.1	aldehyde dehydrogenase 1	830	0	MG	
			NP_00068 0.2	aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1	830	0	MG	
			NP_00387 9.1	aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2	708	0	MG	
			O94788	Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	706	0	MG	
20			NP_00068 4.1	aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6	682	0	MG	
			XP_00701 2.1	similar to Aldehyde dehydrogenase, mitochondrial precursor (ALDH class 2) (ALDH1) (ALDH-E2)	657	0	MG	
			AAA5169 3.1	aldehyde dehydrogenase	656	0	MG	
			6137677	Chain A, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0	MG	
			NP_00068 1.1	aldehyde dehydrogenase 2 family (mitochondrial); aldehyde dehydrogenase 2, mitochondrial	652	0	MG	
25			CAA6829 0.1	precursor polypeptide (AA -36 to 479)	649	0	MG	
			A40872	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 5 precursor, mitochondrial	645	0	MG	
			NP_00068 3.2	aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5	645	0	MG	
			CAD1324 6.1	bA113O24.2 (aldehyde dehydrogenase 1 family, member B1 (ALDH5 ALDHX))	645	0	MG	
			P30837	Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)	642	0	MG	
30			BAA3478 6.1	RALDH2-T	635	0	MG	
			AAH3058 9.1	Similar to aldehyde dehydrogenase 1 family, member A2	622	1.00e- 178	MG	

			I39431	aldehyde dehydrogenase I - human (fragment).	604	1.00e-172	MG	
			AAB5950 0.1	aldehyde dehydrogenase 2 (EC 1.2.1.3)	543	1.00e-154	MG	
			NP_03632 2.2	formyltetrahydrofolate dehydrogenase isoform a	447	1.00e-125	MG	
			O75891	10-formyltetrahydrofolate dehydrogenase (10-FTHFDH)	444	1.00e-124	MG	
			XP_09029 4.1	similar to 10-formyltetrahydrofolate dehydrogenase	431	1.00e-120	MG	
5								
	NM_0187 76 NP_0612 46.1	Mm.339 62 F:(C-HI) -2.07, F:(C-D) -2.11	AAD0242 2.1	cytokine receptor related protein 4	793	0	MG	
10			AAH2356 7.1	cytokine receptor-like factor 3	787	0	MG	
			NP_05707 0.1	cytokine receptor-like molecule 9	786	0	MG	
			XP_06591 0.1	similar to cytokine receptor-like molecule 9	293	1.00e-78	MG	
15								
	NM_0074 74 NP_0315 00.1	Mm.997 0 F:(C-HI) -2.07	NP_00116 0.1	aquaporin 8	354	2.00e-97	MG	
			AAF1905 0.1	aquaporin 8	353	5.00e-97	MG	
20								
	NM_0237 37 NP_0762 26.1	Mm.281 00 F:(C-HI) -2.07	NP_00195 7.1	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	474	1.00e-133	MG	
			AAB1948 2.1	3-hydroxyacyl-CoA dehydrogenase; peroxisomal enoyl-CoA hydratase	366	1.00e-101	MG	
25								
	AK00553 5 BAB2410 6.1	Mm.294 83 F:(C-HI) -2.06, F:(C-D) -2.16	NP_57090 1.1	solute carrier family 39 (zinc transporter), member 4	700	0	MG	
			NP_06023 7.1	solute carrier family 39 (zinc transporter), member 4	578	1.00e-172	MG	
30								
	NM_0098 64 NP_0339 94.1	Mm.356 05 F:(C-HI) -2.05	CAA7935 6.1	E-cadherin	125 3	0	MG	
			NP_00435 1.1	cadherin 1, type 1 preproprotein; calcium-dependent adhesion protein, epithelial; cadherin 1, E-cadherin (epithelial); uvomorulin; cell-CAM 120/80; Arc-1	124 9	0	MG	
			BAA8895 7.1	E-cadherin	123 8	0	MG	
			CAA8458 6.1	E-cadherin	117 9	0	MG	
35			AAA6125 9.1	uvomorulin	115 1	0	MG	
			BAA8895 6.1	E-cadherin	981	0	MG	
			P22223	Cadherin-3 precursor (Placental-cadherin) (P-cadherin)	749	0	MG	

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			NP_00178 4.2	cadherin 3, type 1 preproprotein; P-cadherin; placental cadherin; cadherin 3, P-cadherin (placental); calcium-dependent adhesion protein, placental	746	0	MG	
			P19022	Neural-cadherin precursor (N-cadherin) (Cadherin-2)	581	1.00e-165	MG	
			NP_00178 3.2	cadherin 2, type 1 preproprotein; N-cadherin 1; cadherin 2, N-cadherin (neuronal); neural cadherin; calcium-dependent adhesion protein, neuronal	581	1.00e-165	MG	
			AAB2285 4.1	N-cadherin	581	1.00e-165	MG	
			IJHUCN	cadherin 2 precursor - human	579	1.00e-164	MG	
			AAH3647 0.1	cadherin 2, type 1, N-cadherin (neuronal)	574	1.00e-163	MG	
			NP_00178 5.2	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-cadherin; retinal cadherin	556	1.00e-158	MG	
			P55283	Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-CAD)	540	1.00e-153	MG	
			AAA0323 6.1	N-cadherin	539	1.00e-152	MG	
			CAA4077 3.1	N-cadherin	526	1.00e-148	MG	
			BAC0367 7.1	unnamed protein product	523	1.00e-147	MG	
NM_0233 41 NP_0758 30.1	Mm.283 37	F:(C-HI) -2.05	BAB9136 3.1	chaperone-ABC1-like	702	0	MG	
			BAC1114 3.1	unnamed protein product	700	0	MG	
			NP_06463 2.1	chaperone, ABC1 activity of bc1 complex like	700	0	MG	
			AAH1311 4.2	Similar to RIKEN cDNA 0610012P18 gene	451	1.00e-150	MG	
			NP_07915 2.2	hypothetical protein FLJ12229	449	1.00e-125	MG	
			AAH2747 3.1	Unknown (protein for MGC:36739)	440	1.00e-123	MG	
			AAG1724 5.1	unknown	312	2.00e-84	MG	
AF07106 8 AAC2556 6.1	Mm.129 06	F:(C-HI) -2.04, F:(C-D) -2.29	NP_00078 1.1	dopa decarboxylase (aromatic L-amino acid decarboxylase); aromatic L-amino acid decarboxylase	878	0	MG	
			AAD4048 2.1	aromatic decarboxylase	876	0	MG	
			P19113	Histidine decarboxylase (HDC)	525	1.00e-149	MG	
			NP_00210 3.1	histidine decarboxylase	525	1.00e-149	MG	
NM_0092 63 NP_0332 89.1	Mm.321	F:(C-HI) -2.04	BAC1163 5.1	unnamed protein product	305	2.00e-82	MG	
			P10451	Osteopontin precursor (Bone sialoprotein 1) (Urinary stone protein) (Secreted phosphoprotein 1) (SPP-1) (Nephropontin) (Uropontin)	302	8.00e-82	MG	

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			I56986	OPN-a - human (fragment).	298	2.00e-80	MG	
			NP_00057 3.1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1); Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)	276	8.00e-74	MG	
			I76601	OPN-b - human	270	4.00e-72	MG	
			I76602	OPN-c - human (fragment).	248	2.00e-65	MG	
NM_053200 NP_444430.1	Mm.120807	F:(C-HI) -2.04	NP_03625 4.1	carboxylesterase 3; brain carboxylesterase BR3	1092	0	MG	
			BAB8565 6.1	brain carboxylesterase hBr2	909	0	MG	
			AAH1241 8.1	Unknown (protein for MGC:9220)	908	0	MG	
			NP_00125 7.3	carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)	905	0	MG	
			BAA0465 0.1	carboxylesterase	904	0	MG	
			I61085	carboxylesterase - human	903	0	MG	
			AAD5317 5.1	egasyn	902	0	MG	
			P23141	Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)	902	0	MG	
			AAC6063 1.2	acyl coenzyme A:cholesterol acyltransferase	897	0	MG	
			A48809	carboxylesterase - human	894	0	MG	
			I57004	carboxylesterase - human (fragment).	816	0	MG	
			CAA3714 7.1	serine esterase N-terminal truncated (503 AA)	812	0	MG	
			AAA8393 2.1	carboxylesterase	689	0	MG	
			BAA8499 5.1	brain carboxylesterase hBr1	672	0	MG	
AK007964 BAB25375.1	Mm.21754	F:(C-HI) -2.03, F:(C-D) -2.36	AAH2081 9.1	cholinephosphotransferase 1	604	0	MG	
			NP_06462 9.1	choline phosphotransferase 1; cholinephosphotransferase 1; cholinephosphotransferase 1 alpha	601	0	MG	
			NP_00608 1.1	choline/ethanolaminophosphotransferase	451	1.00e-130	MG	
			AAL3900 5.1	MSTP022	421	1.00e-117	MG	
			AAD4401 9.1	AAPT1-like protein	393	1.00e-109	MG	
			AAF8794 8.1	cholinephosphotransferase 1 beta	320	3.00e-98	MG	
			AAF6119 4.1	PRO1101	283	4.00e-80	MG	

5	NM_0097 48 NP_0338 78.1	Mm.235 64	F:(C-HI) -2.03, F:(C-D) -2.15	NP_00585 9.1	Golgi vesicular membrane trafficking protein p18; Bet1 ( <i>S. cerevisiae</i> ) homolog; Bet1p homolog	194	4.00e- 50	MG	
10	NM_0198 11 NP_0627 85.1	Mm.227 19	F:(C-HI) -2.03, F:(C-D) -2.11	NP_06114 7.1	acetyl-CoA synthetase isoform a; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase	131 4	0	MG	
				AAH1217 2.1	Similar to acetyl-CoA synthetase	131 2	0	MG	
15				BAC0384 9.1	unnamed protein product	130 2	0	MG	
				NP_64480 3.1	acetyl-CoA synthetase isoform b; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase	113 7	0	MG	
20				AAH1014 1.1	Unknown (protein for MGC:19474)	825	0	MG	
				BAB1412 7.1	unnamed protein product	824	0	MG	
25				CAB6178 6.2	dJ18C9.1.1 (similar to acetyl-coenzyme A synthetase, isoform 1)	701	0	MG	
				CAB9342 2.4	dJ1161H23.1 (similar to acetyl-coenzyme A synthetase)	673	0	MG	
30				CAC3303 7.2	dJ18C9.1.2 (similar to acetyl-coenzyme A synthetase, isoform 2)	525	0	MG	
				CAB7550 0.1	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	421	1.00e- 148	MG	
35				XP_04277 0.2	similar to dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	410	1.00e- 117	MG	
				BAC0385 3.1	unnamed protein product	404	1.00e- 112	MG	
				BAB4747 5.1	KIAA1846 protein	335	2.00e- 91	MG	
				NP_07883 6.1	hypothetical protein FLJ21963	325	3.00e- 88	MG	
				CAC3303 9.2	dJ18C9.1.3 (similar to acetyl-coenzyme A synthetase, isoform 3)	218	4.00e- 56	MG	
	NM_0118 34 NP_0359 64.1	Mm.350 20	F:(C-HI) -2.03	NP_05731 2.1	L-kynurenine/alpha-aminoadipate aminotransferase; kynurenine aminotransferase II	669	0	MG	
30				AAH3106 8.1	Similar to L-kynurenine/alpha-aminoadipate aminotransferase	661	0	MG	
	NM_0092 21 NP_0332 47.1	Mm.174 84	F:(C-HI) -2.02	NP_00033 6.1	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor	201	2.00e- 51	MG	
35				AAC0211 4.1	NACP/alpha-synuclein	197	3.00e- 50	MG	
	NM_0111 25 NP_0352 55.1	Mm.610 5	F:(C-HI) -2.01	AAH1984 7.1	phospholipid transfer protein	744	0	MG	

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			NP_00621 8.1	phospholipid transfer protein	744	0	MG	
			CAC3602 0.1	dJ337O18.1.2 (Phospholipid Transfer Protein (Lipid Transfer Protein II) (isoform 2))	634	0	MG	
			AAH0504 5.1	Similar to phospholipid transfer protein	633	0	MG	
NM_0100 62 NP_0341 92.1	Mm.418 53	F:(C-HI) -2.00, F:(C-D) -2.4	NP_00136 6.1	deoxyribonuclease II, lysosomal; DNase II, lysosomal	520	1.00e- 147	MG	
			T45071	hypothetical protein R31240_2 [imported]	494	1.00e- 139	MG	
			NP_06705 6.1	deoxyribonuclease II beta, isoform 1 precursor; DNase II-like acid DNase; endonuclease DLAD	227	5.00e- 59	MG	
			AAL3444 9.1	endonuclease DLAD	227	5.00e- 59	MG	
NM_0078 11 NP_0318 37.1	Mm.422 30	F:(C-HI) -17.03, F:(C-D) -3.81	NP_00077 4.2	cytochrome P450, subfamily XXVIA, polypeptide 1, isoform 1; P450, retinoic acid-inactivating, 1; retinoic acid-metabolizing cytochrome; retinoic acid 4-hydroxylase	901	0	MG	
			O43174	Cytochrome P450 26 (Retinoic acid-metabolizing cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase)	896	0	MG	
			NP_47649 8.1	cytochrome P450, subfamily XXVIA, polypeptide 1, isoform 2; P450, retinoic acid-inactivating, 1; retinoic acid-metabolizing cytochrome; retinoic acid 4-hydroxylase	813	0	MG	
			NP_06393 8.1	cytochrome P450 retinoid metabolizing protein	391	e-108	MG	
NM_0532 15 NP_4444 45.1	Mm.160 362	F:(C-HI) -1.98, F:(C-D) -3.23	NP_00106 8.1	UDP glycosyltransferase 2 family, polypeptide B17; UDP-glucuronosyltransferase, family 2, beta-17	728	0	MG	
			XP_01109 7.5	similar to UDP-glucuronosyltransferase 2B15 precursor, microsomal (UDPGT) (UDPGTH-3) (HLUG4)	715	0	MG	
			NP_00106 7.1	UDP glycosyltransferase 2 family, polypeptide B15; UDP-glucuronosyltransferase, family 2, beta-15	715	0	MG	
			AAD5509 3.1	UDP-glucuronosyltransferase 2B15	712	0	MG	
			XP_05034 5.4	similar to UDP-glucuronosyltransferase 2B4 precursor, microsomal (UDPGT) (Hydroxycholeic acid) (HLUG25) (UDPGTH-1)	705	0	MG	
			AAC9500 2.1	UDP-glucuronosyltransferase 2B4 precursor	703	0	MG	
			JN0619	glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human	702	0	MG	
			AAC3227 2.1	UDP glucuronosyltransferase 2B4 precursor	697	0	MG	
			NP_00106 5.1	UDP glycosyltransferase 2 family, polypeptide B7; UDP-glucuronosyltransferase, family 2, beta-7	692	0	MG	
			SI1309	glucuronosyltransferase (EC 2.4.1.17) - human	691	0	MG	
			AAH3097 4.1	UDP glycosyltransferase 2 family, polypeptide B7	690	0	MG	
			NP_06696 2.1	UDP glycosyltransferase 2 family, polypeptide B4; UDP-glucuronosyltransferase, family 2, beta-4	688	0	MG	
			NP_00106 4.1	UDP glycosyltransferase 2 family, polypeptide B11	677	0	MG	

			JE0200	orphan UDP-glucuronosyltransferase (EC 2.4.-.-)	677	0	MG	
			NP_00106 6.1	UDP glycosyltransferase 2 family, polypeptide B10	660	0	MG	
			NP_44426 7.1	UDP glycosyltransferase 2 family, polypeptide B28	660	0	MG	
			NP_00678 9.1	UDP glycosyltransferase 2 family, polypeptide A1; UDP glucuronosyltransferase 2 family, polypeptide A1	579	1.00e-165	MG	
5	NM_0099 93 NP_0341 23.1	Mm.155 37 F:(C-D) -3.27	AAK2572 8.1	cytochrome P450	778	0	MG	
10			NP_00075 2.1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase	775	0	MG	
			AAF1359 9.1	cytochrome P450-1A2	774	0	MG	
			AAA3573 8.1	cytochrome P450 4	773	0	MG	
			NP_00049 0.1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	705	0	MG	
			AAA5213 9.1	cytochrome P-450-1	703	0	MG	
15			CAA2645 8.1	cytochrome P(1)-450	703	0	MG	
			XP_04466 0.4	similar to CYTOCHROME P450 1A2 (CYP1A2) (P450-P3) (P(3)450) (P450 4)	558	1.00e-158	MG	
			AAC5080 9.1	cytochrome P450 CYP1B1	349	5.00e-98	MG	
			NP_00009 5.1	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	349	5.00e-98	MG	
20	NM_0077 06 NP_0317 32.1	Mm.413 2 F:(C-D) -2.51	NP_00386 8.1	suppressor of cytokine signaling-2; STAT induced STAT inhibitor-2; cytokine-inducible SH2 protein 2	364	1.00e-100	MG	
			JC5626	STAT induced STAT inhibitor 2 - human	361	1.00e-100	MG	
			JC5760	cytokine-inducible SH2 protein 2 - human	360	3.00e-99	MG	
25			BAA2253 6.1	CIS2	359	3.00e-99	MG	
			AAC9889 6.1	suppressor of cytokine signaling-2; HSSOCS-2	350	3.00e-98	MG	
	NM_0093 96 NP_0334 22.1	Mm.434 8 F:(C-D) -2.5	NP_00628 2.1	tumor necrosis factor, alpha-induced protein 2	790	0	MG	



5	AK00492 4 BAB2367 5.1	Mm.278 89	F:(C-D) -2.42	XP_05875 3.1	similar to coenzyme A diphosphatase	300	7.00e-81	MG	
	NM_0298 13 NP_0840 89.1	Mm.159 813	F:(C-D) -2.4	NP_68981 4.1	hypothetical protein FLJ38281	373	1.00e-103	MG	
10				XP_09196 0.1	similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	373	1.00e-103	MG	
				NP_06635 8.1	zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	364	1.00e-100	MG	
15				NP_69918 9.1	hypothetical protein FLJ90396	364	1.00e-100	MG	
				XP_09195 8.1	similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	364	1.00e-100	MG	
20				XP_09196 8.4	similar to zinc finger protein 91 (HPF7, HTF10)	353	6.00e-97	MG	
				AAF7179 0.1	ZNF180	347	6.00e-95	MG	
25				NP_03738 8.1	zinc finger protein 180 (HHZ168)	347	6.00e-95	MG	
				NP_00342 8.1	zinc finger protein 136 (clone pHZ-20)	345	1.00e-94	MG	
30				NP_68981 5.1	hypothetical protein FLJ40981	344	3.00e-94	MG	
				NP_08511 6.1	hypothetical protein FLJ21628	343	8.00e-94	MG	
				AAD2360 7.1	BC37285_1	341	2.00e-93	MG	
				BAC0430 9.1	unnamed protein product	338	2.00e-92	MG	
				BAB2180 1.1	KIAA1710 protein	337	3.00e-92	MG	
				XP_03281 2.1	similar to hypothetical protein FLJ40981	337	3.00e-92	MG	
				XP_03128 3.1	similar to Hypothetical zinc finger protein KIAA1710	337	3.00e-92	MG	
				P35789	Zinc finger protein 93 (Zinc finger protein HTF34)	336	8.00e-92	MG	
				NP_00342 7.1	zinc finger protein 135 (clone pHZ-17)	336	1.00e-91	MG	
				NP_65329 0.2	hypothetical protein FLJ32191	335	1.00e-91	MG	
				BAB7125 7.1	unnamed protein product	333	8.00e-91	MG	
				BAC0476 4.1	unnamed protein product	332	2.00e-90	MG	
				NP_00342 0.1	zinc finger protein 85 (HPF4, HTF1)	330	5.00e-90	MG	
				BAA8651 2.1	KIAA1198 protein	328	3.00e-89	MG	
				XP_03267 4.1	similar to Hypothetical zinc finger protein KIAA1198	328	3.00e-89	MG	
				NP_66033 8.1	similar to Zinc finger protein 136	327	4.00e-89	MG	

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			BAB7127 2.1	unnamed protein product	327	6.00e -89	MG	
			XP_06538 7.2	similar to Zinc finger protein 135	326	1.00e -88	MG	
			XP_08607 0.1	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	325	1.00e -88	MG	
			NP_00342 1.1	zinc finger protein 91 (HPF7, HTF10)	325	1.00e -88	MG	
			XP_06853 8.2	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	325	2.00e -88	MG	
			XP_02831 4.1	similar to KRAB zinc finger protein KR18	324	3.00e -88	MG	
			XP_11565 8.2	similar to Zinc finger protein 208	324	3.00e -88	MG	
			T14757	hypothetical protein DKFZp572C163.1 - human (fragment)	324	3.00e -88	MG	
			XP_09198 3.1	similar to Zinc finger protein 135	324	4.00e -88	MG	
			CAB9423 2.2	zinc finger protein	323	5.00e -88	MG	
			NP_00341 9.1	zinc finger protein 84 (HPF2)	323	5.00e -88	MG	
			B32891	finger protein 2, placental - human	323	5.00e -88	MG	
			NP_05529 5.1	zinc finger protein AF020591	323	7.00e -88	MG	
			AAC5118 0.1	kruppel-related zinc finger protein	323	9.00e -88	MG	
			XP_09209 7.1	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	322	1.00e -87	MG	
			AAH3611 0.1	Similar to zinc finger protein 208	322	1.00e -87	MG	
			BAC0461 0.1	unnamed protein product	322	2.00e -87	MG	
			NP_61214 3.1	hypothetical protein FLJ31526	322	2.00e -87	MG	
			NP_06703 9.1	zinc finger protein 71; endothelial zinc finger . protein induced by tumor necrosis factor alpha	321	3.00e -87	MG	
			NP_00339 9.1	zinc finger protein 37 homolog (mouse); Zinc finger protein-37, mouse, homolog of; zinc finger protein homologous to Zfp37 in mouse	321	3.00e -87	MG	
			BAC0406 4.1	unnamed protein product	321	3.00e -87	MG	
			Q9Y6Q3	Zinc finger protein ZFP-37	321	3.00e -87	MG	
			AAD2360 8.1	BC37295_2 (partial)	321	3.00e -87	MG	
			AAL5844 2.1	zinc finger protein 328	321	3.00e -87	MG	
			BAB4748 1.1	KIAA1852 protein	321	3.00e -87	MG	
			AAH3720 9.1	Unknown (protein for MGC:41936)	320	4.00e -87	MG	
			XP_17175 2.1	similar to zinc finger protein 29	320	4.00e -87	MG	
			XP_09209 0.2	similar to Hypothetical zinc finger protein KIAA1473	320	6.00e -87	MG	
			BAA2405 0.1	Zinc-finger protein	320	6.00e -87	MG	

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			NP_44309 2.1	kruppel-like zinc finger protein	319	1.00e -86	MG	
			XP_17194 0.1	similar to BC37295_1	318	2.00e -86	MG	
			NP_65329 4.1	hypothetical protein FLJ30932	318	2.00e -86	MG	
			XP_06492 9.5	similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)	318	2.00e -86	MG	
			NP_07900 9.1	hypothetical protein FLJ14345	318	2.00e -86	MG	
			NP_00341 6.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain	318	2.00e -86	MG	
			AAF6303 0.1	Zinc finger protein ZNF45	318	2.00e -86	MG	
			NP_00888 9.1	zinc finger protein 16 (KOX 9)	318	2.00e -86	MG	
			CAD3911 1.1	hypothetical protein	318	2.00e -86	MG	
			XP_09209 3.1	similar to Zinc finger protein 85	318	2.00e -86	MG	
			P17020	Zinc finger protein 16 (Zinc finger protein KOX9)	318	2.00e -86	MG	
			AAH0652 8.1	zinc finger protein 43 (HTF6)	318	3.00e -86	MG	
			XP_08612 8.1	similar to Zinc finger protein 35 (Zfp-35)	318	3.00e -86	MG	
			XP_06511 6.3	similar to zinc finger protein 91 (HPF7, HTF10)	317	4.00e -86	MG	
			NP_00341 4.1	zinc finger protein 43 (HTF6)	317	4.00e -86	MG	
			AAH3557 9.1	Similar to zinc finger protein 208	317	4.00e -86	MG	
			NP_06112 1.1	zinc finger protein ZFP	317	5.00e -86	MG	
			NP_00344 2.1	zinc finger protein 177	317	5.00e -86	MG	
			XP_08750 3.1	similar to zinc finger protein 91 (HPF7, HTF10)	317	5.00e -86	MG	
			XP_03388 8.3	similar to Zinc finger protein 41	317	6.00e -86	MG	
			CAC8816 2.1	bB479F17.3 (zinc finger protein 41)	317	6.00e -86	MG	
			NP_70035 9.1	zinc finger protein 41	317	6.00e -86	MG	
			A54661	zinc finger protein ZNF41 - human (fragment)	317	6.00e -86	MG	
			AAH2299 2.1	Unknown (protein for MGC:29879)	317	6.00e -86	MG	
			XP_16636 7.1	similar to Zinc finger protein 184	317	6.00e -86	MG	
			BAC0421 6.1	unnamed protein product	316	8.00e -86	MG	
			NP_06570 4.1	zinc finger protein 287	316	8.00e -86	MG	
			NP_06102 5.3	zinc finger protein 331; zinc finger protein 463; C2H2-like zinc finger protein	315	1.00e -85	MG	

			AAF7807 5.1	KRAB zinc finger protein	315	1.00e -85	MG	
			AAH3671 4.1	Unknown (protein for IMAGE:4846514)	315	2.00e -85	MG	
			T12489	hypothetical protein DKFZp572P0920.1 - human (fragment)	315	2.00e -85	MG	
			XP_03281 0.1	similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)	315	2.00e -85	MG	
5			AAF8810 7.1	Hypothetical zinc finger-like protein	315	2.00e -85	MG	
			NP_61220 3.1	TRAF8-inhibitory zinc finger protein; TRAF8-binding zinc finger protein	314	3.00e -85	MG	
			XP_09208 8.3	similar to zinc finger protein 91 (HPF7, HTF10)	314	3.00e -85	MG	
			XP_04755 4.4	similar to Hypothetical zinc finger protein KIAA1473	314	4.00e -85	MG	
			NP_00662 0.1	zinc finger protein 271	313	5.00e -85	MG	
10			Q9P255	Hypothetical zinc finger protein KIAA1473	313	9.00e -85	MG	
			BAB8554 2.1	KIAA1956 protein	313	9.00e -85	MG	
			XP_08583 6.1	similar to Hypothetical zinc finger protein KIAA1956	313	9.00e -85	MG	
			XP_04755 0.1	similar to Hypothetical zinc finger protein KIAA1473	313	9.00e -85	MG	
			NP_00340 6.1	zinc finger protein 268	312	1.00e -84	MG	
15			AAH3603 8.1	Unknown (protein for MGC:33240)	312	1.00e -84	MG	
			AAK6930 7.1	ZNF268B	312	1.00e -84	MG	
			S47071	finger protein HZF3, Krueppel-related - human (fragment)	312	2.00e -84	MG	
			NP_03751 2.1	zinc finger protein 228	312	2.00e -84	MG	
20	NM_0074 94 NP_0315 20.1	Mm.321 7 F:(C-D) -2.36	NP_44646 4.1	argininosuccinate synthetase				
					793	0	MG	
			NP_00004 1.1	argininosuccinate synthetase	781	0	MG	
			XP_09449 3.2	similar to argininosuccinate synthetase	612	1.00e- 175	MG	
25			XP_16727 7.1	similar to argininosuccinate synthetase	602	1.00e- 172	MG	
			XP_06201 0.1	similar to argininosuccinate synthetase	601	1.00e- 172	MG	
			XP_09454 2.1	similar to argininosuccinate synthetase	410	1.00e- 114	MG	
			XP_17241 9.1	similar to argininosuccinate synthetase	305	9.00e- 83	MG	
			XP_09598 9.1	similar to argininosuccinate synthetase	253	4.00e- 67	MG	
30			AAB9632 8.1	argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	231	2.00e- 60	MG	
			XP_07011 6.1	similar to argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	218	2.00e- 56	MG	

			XP_07092 8.1	similar to argininosuccinate	211	2.00e- 54	MG	
5	NM_0087 92 NP_0328 18.1	Mm.124 7 F:(C-D) -2.35	NP_00258 5.2	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5	124 7	0	MG	
			AAA6003 2.1	endoprotease	124 4	0	MG	
			CAB8942 8.1	dJ531H16.1 (proprotein convertase subtilisin/kexin type 2 (NEC2))	892	0	MG	
10	AK01078 6 BAB2718 2.1	Mm.200 858 F:(C-D) -2.27	AAH0135 2.1	tubulin, beta polypeptide	838	0	MG	
			T08726	tubulin beta chain - human	835	0	MG	
			NP_00106 0.1	tubulin, beta polypeptide	833	0	MG	
			NP_00607 9.1	tubulin, beta, 2	830	0	MG	
15			AAH2403 8.1	Similar to tubulin, beta, 2	828	0	MG	
			AAH2952 9.1	tubulin, beta, 2	827	0	MG	
			P05218	Tubulin beta-5 chain	823	0	MG	
			AAH2094 6.1	tubulin, beta 5	822	0	MG	
			NP_00607 8.2	tubulin, beta, 5	820	0	MG	
20			P07437	Tubulin beta-1 chain	815	0	MG	
			P04350	Tubulin beta-5 chain	813	0	MG	
			O808321A	tubulin beta	813	0	MG	
			I38369	beta-tubulin - human (fragment)	801	0	MG	
			AAH0302 1.1	Unknown	795	0	MG	
25			Q13509	Tubulin beta-4 chain (Tubulin beta-III)	794	0	MG	
			NP_00607 7.1	tubulin, beta, 4	793	0	MG	
			XP_04708 3.4	similar to neu differentiation factor - human (fragment)	789	0	MG	
			BAB1401 6.1	unnamed protein product	785	0	MG	
			NP_11591 4.1	similar to chicken tubulin beta 5	785	0	MG	
30			AAL3243 4.1	beta-tubulin 4Q	775	0	MG	
			O805287A	tubulin beta	770	0	MG	
			XP_04743 6.3	similar to tubulin, beta 3	756	0	MG	
			NP_06442 4.1	tubulin, beta polypeptide 4, member Q	731	0	MG	
			AAB4845 6.1	beta-tubulin	726	0	MG	
35			AAH0167 8.1	Unknown (protein for IMAGE:2821278)	708	0	MG	
			NP_11040 0.1	beta tubulin 1, class VI	691	0	MG	

			XP_02757 7.1	similar to beta-tubulin 4Q	644	0	MG	
NM_0081 83 NP_0322 09.1	Mm.146 01	F:(C-D) -2.27	XP_00215 5.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)	395	1.00e -110		
			4388890	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a	394	1.00e -109	MG	
			AAA5920 3.1	glutathione transferase M1	394	1.00e -109	MG	
			NP_00083 9.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-aralkyltransferase M2	379	1.00e -105		
			P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	379	1.00e -105	MG	
			NP_00084 2.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-aralkyltransferase M5; GST class-mu 5	378	1.00e -105		
			NP_00084 1.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-aralkyltransferase M4; GTS-Mu2; GST class-mu 4	377	1.00e -104		
			S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2) - human	377	1.00e -104	MG	
			4537966	ain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	377	1.00e -104		
			AAA5734 6.1	glutathione transferase M4	376	1.00e -104	MG	
			6980588	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	376	1.00e -104	MG	
			494185	Chain , Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214F)	373	1.00e -103		
			CAA4863 6.1	glutathione S-transferase	351	8.00e -97	MG	
			NP_67148 9.1	glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-aralkyltransferase M4; GTS-Mu2; GST class-mu 4	340	2.00e -93		
			AAH1783 6.1	Similar to glutathione S-transferase M2 (muscle)	338	7.00e -93	MG	
			XP_04272 2.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	329	3.00e -90	MG	
			AAH0879 0.1	Unknown (protein for MGC:3704)	329	3.00e -90	MG	
			5822511	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	329	3.00e -90		

			106129	glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human	326	3.00e-89	MG	
			NP_666533.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu	308	1.00e-83		MG
5	NM_012006 NP_036136.1	Mm.1978 F:(C-D) -2.24	XP_170752.1	similar to peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein	602	1.00e-172	MG	
			P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)	600	1.00e-171	MG	
			AAH06500.1	Unknown (protein for MGC:2366)	600	1.00e-171	MG	
			NP_006812.2	peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein	599	1.00e-171	MG	
10			BAA91989.1	unnamed protein product	598	1.00e-171	MG	
			NP_689544.1	hypothetical protein FLJ31235	494	1.00e-139	MG	
			AAC42007.1	ORF; putative	405	1.00e-113	MG	
			XP_090885.1	similar to Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)	280	4.00e-75	MG	
15	AK006569 BAB24656.1	Mm.45980 F:(C-D) -2.18	NP_060301.1	hypothetical protein FLJ20456	254	6.00e-70	MG	
			AAH12021.1	Unknown (protein for MGC:21737)	245	5.00e-67	MG	
20	NM_010107 NP_034237.1	Mm.15675 F:(C-D) -2.18	NP_004419.1	ephrin A1 precursor; eph-related receptor tyrosine kinase ligand 1 (tumor necrosis factor, alpha-induced protein 4)	353	2.00e-97	MG	
			AAH32698.1	ephrin-A1	351	8.00e-97	MG	
25	NM_025754 NP_080030.1	Mm.20213 F:(C-D) -2.13	NP_000025.1	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase	647	0	MG	
			229674	Chain , Aldolase A (E.C.4.1.2.13)	645	0	MG	
			CAA30979.1	aldolase A	636	0	MG	
30			NP_005156.1	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase	556	1.00e-158	MG	
			CAA30270.1	aldolase C	555	1.00e-158	MG	
35	NM_008303 NP_032329.1	Mm.197601 F:(C-D) -2.12	NP_002148.1	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (chaperonin 10)	171	3.00e+43	MG	

5	NM_011300 NP_035430.1	Mm.5281	F:(C-D) -2.11	NP_001002.1	ribosomal protein S7; 40S ribosomal protein S7				
						376	1.00e-104	MG	
					AAB00969.1	ribosomal protein	372	1.00e-103	MG
					XP_012638.7	similar to bA271B5.1 (similar to ribosomal protein S7)	368	1.00e-102	MG
					CAC17691.1	bA271B5.1 (similar to ribosomal protein S7)	368	1.00e-102	MG
					XP_015712.4	similar to ribosomal protein S7	352	3.00e-97	MG
					XP_056970.1	similar to ribosomal protein S7	341	5.00e-94	MG
					XP_066966.1	similar to ribosomal protein S7	297	1.00e-80	MG
					XP_068930.1	similar to ribosomal protein S7	290	2.00e-78	MG
					XP_170827.1	similar to ribosomal protein S7	273	1.00e-73	MG
10					XP_117815.2	similar to ribosomal protein S7	236	2.00e-62	MG
					AK011896 BAB27902.1	unnamed protein product			
					BAB14594.1		213	5.00e-55	MG
					CAB66586.2	hypothetical protein	211	3.00e-54	MG
					NM_008322 NP_032348.1	isocitrate dehydrogenase [NADP], mitochondrial precursor (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) (ICD-M)	850	0	MG
					NP_002159.1		845	0	MG
					AAC50455.1		734	0	MG
					XP_028869.1		566	1.00e-161	MG
					NP_005887.1		566	1.00e-161	MG
					T46280		565	1.00e-161	MG
					XP_068996.1		436	1.00e-122	MG
					NM_011802 NP_035932.1	ClpX caseinolytic protease X homolog; energy-dependent regulator of proteolysis; ClpX (caseinolytic protease X, E. coli)	104	0	MG
					CAB66856.1		856	0	MG
35	AK004138 BAB23187.1	Mm.29364	F:(C-D) -2.06	CAA36480.1	ORFII				
						125	1.00e-65	HG	
					NP_060110.1	hypothetical protein FLJ20048	243	8.00e-61	HG



			AAC5126 9.1	putative p150	126	5.00e- 52	HG	
			AAC5127 1.1	putative p150	129	3.00e- 51	HG	
			AAC5127 6.1	putative p150	127	3.00e- 51	HG	
			AAA8803 7.1	unknown protein	127	3.00e- 51	HG	
5	NM_0085 09 NP_0325 35.1	Mm.151 4 F:(C-D) -2.05, F:(HI-D) -2.42	NP_00022 8.1	lipoprotein lipase precursor	838	0	MG	
			AAH1135 3.1	Similar to lipoprotein lipase	836	0	MG	
10			AAC6167 9.1	lipoprotein lipase precursor	602	1.00e- 170	MG	
			NP_00602 4.1	endothelial lipase precursor; endothelial cell-derived lipase	436	1.00e- 120	MG	
			NP_00022 7.1	lipase C precursor	380	1.00e- 103	MG	
			AAA5952 0.1	hepatic lipase precursor	379	1.00e- 103	MG	
			A28997	triacylglycerol lipase (EC 3.1.1.3) precursor, hepatic	379	1.00e- 103	MG	
15	NM_0135 41 NP_0385 69.1	Mm.426 F:(C-D) -2.05	5822569	Chain A, Crystal Structure Of Hgstp1-1[v104] Complexed With The Gsh Conjugate Of (+)-Anti-Bpde	377	1.00e- -105	MG	
			2554839	Chain A, Crystal Structure Of Human Glutathione S-Transferase P1-1[v104] Complexed With S-Hexylglutathione	377	1.00e- -104	MG	
20			AAC1386 9.1	glutathione S-transferase-P1c	376	1.00e- -104	MG	
			NP_00084 3.1	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester synthase III	376	1.00e- -104	MG	
			4699783	Chain A, Human Glutathione S-Transferase P1-1 Y49f Mutant	375	1.00e- -104	MG	
			CAA3089 4.1	glutathione S-transferase	374	1.00e- -104	MG	
			2981694	Chain A, Glutathione S-Transferase In Complex With Glutathione	374	1.00e- -104	MG	
25			4139536	Chain A, Glutathione S-Transferase P1-1	374	1.00e- -104	MG	
			2914230	Chain A, Human Glutathione S-Transferase P1-1 Y108f Mutant	373	1.00e- -103	MG	
			23200508	Chain A, A Folding Mutant Of Human Class Pi Glutathione Transferase, Created By Mutating Glycine 146 Of The Wild-Type Protein To Alanine	372	1.00e- -103	MG	
			2780951	Chain A, Glutathione S-Transferase In Complex With P-Bromobenzylglutathione	372	1.00e- -103	MG	
			11514451	Chain A, Glutathione Transferase P1-1	371	1.00e- -103	MG	
30			23200510	Chain A, A Folding Mutant Of Human Class Pi Glutathione Transferase, Created By Mutating Glycine 146 Of The Wild-Type Protein To Valine	371	1.00e- -103	MG	
			11514448	Chain A, Crystal Structure Of Pi Class Glutathione Transferase	370	1.00e- -103	MG	

			A41177	glutathione transferase (EC 2.5.1.18) / fatty-acyl-ethyl-ester synthase (EC 3.1.1.67) III, myocardial	368	1.00e-102	MG	
			20664358	Chain A, Crystal Structure Of A Recombinant Glutathione Transferase, Created By Replacing The Last Seven Residues Of Each Subunit Of The Human Class Pi Isoenzyme With The Additional C-Terminal Helix Of Human Class Alpha Isoenzyme	360	1.00e-100	MG	
			A60445	glutathione transferase (EC 2.5.1.18) pi - human	309	2.00e-84	MG	
5	NM_0087 56 NP_0327 82.1	Mm.480 7 F:(C-D) -2.04	NP_00252 9.1	occludin	899	0	MG	
			AAH2988 6.1	occludin	897	0	MG	
10	NM_0093 49 NP_0333 75.1	Mm.299 F:(C-D) -2.04	AAD0472 3.1	thioether S-methyltransferase-like; similar to P40936 (PID:g731019)	271	8.00e-73	MG	
			O95050	Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)	267	2.00e-71	MG	
			NP_00676 5.3	indolethylamine N-methyltransferase; thioester S-methyltransferase-like	266	5.00e-71	MG	
15			AAH3381 3.1	Unknown (protein for IMAGE:5209218)	266	5.00e-71	MG	
			NP_00616 0.1	nicotinamide N-methyltransferase	239	6.00e-63	MG	
20	NM_0238 50 NP_0763 39.1	Mm.380 21 F:(C-D) -2.03	NP_00364 5.1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1; carbohydrate (chondroitin 6/keratan) sulfotransferase 1	778	0	MG	
			NP_00426 4.2	carbohydrate (chondroitin 6) sulfotransferase 3; chondroitin 6-sulfotransferase	305	1.00e-82	MG	
			BAA3257 6.1	chondroitin 6-sulfotransferase	303	7.00e-82	MG	
			NP_06762 8.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6; macular dystrophy, corneal, 1; carbohydrate sulfotransferase 6; corneal N-acetylglucosamine 6-sulfotransferase	214	4.00e-55	MG	
			NP_00576 0.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4; N-acetylglucosamine 6-O-sulfotransferase	209	1.00e-53	MG	
25			AAH3528 2.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	209	1.00e-53	MG	
			BAC1117 7.1	unnamed protein product	209	2.00e-53	MG	
30	NM_0331 46 NP_1491 58.1	Mm.406 67 F:(C-D) -2.03	Q9Y3B6	Protein CGI-112	393	1.00e-109	MG	
			NP_05713 3.1	CGI-112 protein	390	1.00e-108	MG	

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			XP_03333 2.4	similar to Protein CGI-112	388	1.00e- 108	MG	
NM_0103 24 NP_0344 54.1	Mm.190 39	F:(C-D) -2.01	S29028	aspartate transaminase (EC 2.6.1.1) (clone 8C7)	810	0	MG	
			S13035	aspartate transaminase (EC 2.6.1.1) - human	779	0	MG	
			NP_00207 0.1	aspartate aminotransferase 1; glutamic-oxaloacetic transaminase 1, soluble	779	0	MG	
			AAH0052 5.1	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	395	1.00e- 109	MG	
NM_0169 78 NP_0586 74.1	Mm.136 94	F:(C-D) -2.01	NP_00026 5.1	ornithine aminotransferase precursor; Ornithine aminotransferase	781	0	MG	
			AAB3521 1.1	ornithine aminotransferase, OAT [human, gyrate atrophy of the choroid and retina (GACR) patient, Peptide Mutant, 439 aa]	780	0	MG	
			3319072	Chain A, Human Ornithine Aminotransferase Complexed With The Neurotoxin Gabaculine	727	0	MG	
			XP_09301 5.1	ar to Ornithine aminotransferase, mitochondrial precursor (Ornithine-oxo-acid aminotransferase)	393	e-109	MG	
NM_0111 72 NP_0353 02.1	Mm.284 56	F:(C-D) -2	NP_05741 9.2	proline dehydrogenase (oxidase) 1; proline oxidase 2; p53 induced protein	889	0	MG	
			AAF2146 4.1	proline oxidase 2	888	0	MG	
			AAD2477 5.1	proline dehydrogenase; PRODH	822	0	MG	
			NP_00596 5.1	proline dehydrogenase; proline oxidase 2	821	0	MG	
			BAB3332 3.1	KIAA1653 protein	239	9.00e- 63	MG	
			NP_06705 5.1	kidney and liver proline oxidase 1	200	6.00e- 51	MG	
NM_0138 09 NP_0388 37.1	Mm.102 312	F:(C-D) -2	NP_00075 7.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	563	1.00e- 159	MG	
			Q16696	Cytochrome P450 2A13 (CYP1A13)	558	1.00e- 158	MG	
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 -	555	1.00e- 158	MG	
			NP_00075 3.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	553	1.00e- 157	MG	
			P11509	Cytochrome P450 2A6 (CYP1A6) (Coumarin 7-hydroxylase) (IIA3) (CYP2A3) (P450(I))	552	1.00e- 157	MG	
			AAF1360 0.1	cytochrome P450-2A6	551	1.00e- 157	MG	
			I609083A	cytochrome P450IIA	551	1.00e- 156	MG	
			CAA3209 7.1	cytochrome P-450IIA (AA 1 - 489)	551	1.00e- 156	MG	

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		P20853	Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)	543	1.00e-154	MG	
		C34271	cytochrome P450 2A4 - human	543	1.00e-154	MG	
		NP_000755.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 1	540	1.00e-153	MG	
		I38965	cytochrome P450 - human	540	1.00e-153	MG	
		I38967	cytochrome P450 - human	529	1.00e-150	MG	
		CAA32117.1	P-450 IIA3 protein (1 is 3rd base in codon)	518	1.00e-146	MG	
		NP_000765.2	cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily IIF, polypeptide 1 (H. sapiens)	516	1.00e-146	MG	
		NP_000758.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	516	1.00e-146	MG	
		NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	514	1.00e-145	MG	
		AAB23864.2	cytochrome P-450	514	1.00e-145	MG	
		BAA00123.1	cytochrome P-450	514	1.00e-145	MG	
		P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	512	1.00e-145	MG	
		AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	512	1.00e-145	MG	
		NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	511	1.00e-144	MG	
		P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	511	1.00e-144	MG	
		AAH20596.1	Unknown (protein for MGC:22146)	509	1.00e-144	MG	
		AAL69652.1	cytochrome P450 2F1	509	1.00e-144	MG	
		AAF13602.1	cytochrome P450-2B6	509	1.00e-144	MG	
		I506290A	cytochrome P450	509	1.00e-144	MG	
		NP_000761.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	508	1.00e-144	MG	
		AAA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	507	1.00e-143	MG	
		S66382	cytochrome P450 2C8 - human	506	1.00e-143	MG	

			AAB3529 2.1	cytochrome P450 arachidonic acid epoxigenase Isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	506	1.00e- 143	MG	
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	506	1.00e- 143	MG	
			NP_00076 3.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	502	1.00e- 142	MG	
			AAAS216 1.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	502	1.00e- 142	MG	
5			P33260	ome P450 2C18 (CYP11C18) (P450-6B/29C)	500	1.00e- 141	MG	
			P24903	Cytochrome P450 2F1 (CYP11F1)	496	1.00e- 140	MG	
			I52418	cytochrome P450 - human	475	1.00e- 133	MG	
			I38966	cytochrome P450 - human	467	1.00e- 131	MG	
			NP_00076 4.1	cytochrome P450, subfamily IIE, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)	464	1.00e- 130	MG	
10			AAF1360 1.1	cytochrome P450-2E1	464	1.00e- 130	MG	
			AAD1375 3.1	cytochrome P450 2E1	460	1.00e- 129	MG	
			NP_08512 5.1	cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P540, subfamily IIS, polypeptide 1	455	1.00e- 127	MG	
			BAB5522 7.1	unnamed protein product	451	1.00e- 126	MG	
			NP_08507 9.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 Isoform 2	445	1.00e- 125	MG	
15			AAAS215 9.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	418	1.00e- 116	MG	
			NP_11051 8.1	cytochrome P450, subfamily IIC, polypeptide 8 Isoform 2; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	406	1.00e- 113	MG	
			G38462	cytochrome P450 2C17 - human (fragment)	404	1.00e- 112	MG	
			AAAS214 3.1	cytochrome P450-IIB	389	1.00e- 108	MG	
			S21423	cytochrome P450 2C - human	382	1.00e- 106	MG	
20			NP_00076 6.2	cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase; Cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase).	367	1.00e- 101	MG	
			BAB8548 9.1	cytochrome P450 2J2	367	1.00e- 101	MG	
			O4HUPB	cytochrome P450 2A3, hepatic - human	329	9.00e- 90	MG	

			AAA5350 0.1	cytochrome P450 IID6	313	7.00e- 85	MG	
			NP_00009 7.1	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	311	2.00e- 84	MG	
NM_0081 84 NP_0322 10.1	Mm.310 41	F:(C-D) -1.78	AAA5920 3.1	glutathione transferase M1	342	3.00e- 93	MG	
			XP_00215 5.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)	341	4.00e- 93	MG	
			pdb 1GTU 	Glutathione S-Transferase; Chain: A, B, C, D; Ec: 2.5.1.18	339	1.00e- 92	MG	
			NP_00083 9.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	334	6.00e- 91	MG	
			pdb 2GTU 	Glutathione S-Transferase; Chain: A, B; Ec: 2.5.1.18	332	2.00e- 90	MG	
			pdb 1HNA 	Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C. 2.5.1.18) Mutant With Trp 214	328	3.00e- 89	MG	
			NP_00084 1.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	326	1.00e- 88	MG	
			P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	325	2.00e- 88	MG	
			AAA5734 6.1	glutathione transferase M4	325	3.00e- 88	MG	
			S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2) - human	325	3.00e- 88	MG	
			pdb 4GTU 	Glutathione S-Transferase; Chain: A, B, C, D, E, F, G, H; Ec: 2.5.1.18	325	4.00e- 88	MG	
			NP_00084 2.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	324	5.00e- 88	MG	
			CAA4863 6.1	glutathione S-transferase	296	1.00e- 79	MG	
			AAH1783 6.1	Similar to glutathione S-transferase M2 (muscle)	289	2.00e- 77	MG	
			pdb 3GTU 	Glutathione S-Transferase; Chain: A, B, C, D; Ec: 2.5.1.18	288	3.00e- 77	MG	
			XP_04272 2.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	288	3.00e- 77	MG	
			AAH0879 0.1	Unknown (protein for MGC:3704)	288	3.00e- 77	MG	
			A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human	285	2.00e- 76	MG	

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			NP_67148 9.1	glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	283	2.00e -75		
			XP_16702 3.1	similar to glutathione transferase M2 [Macaca fuscata]	257	7.00e -68	MG	
			NP_66653 3.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	256	1.00e -67		
AK00379 7 BAB2300 1.1	Mm.282 52	F:(C-D) -1.71	CAD3914 0.1	hypothetical protein				
			AAH1207 9.1	Similar to molybdenum cofactor sulfurase	319	2.00e -86	MG	
			NP_06041 7.1	molybdenum cofactor sulfurase	319	2.00e -86	MG	
					316	2.00e -85	MG	
S80191 AAB2133 5.1		F:(C-D) -1.61	AAH1241 8.1	Unknown (protein for MGC:9220)	828	0		
			NP_00125 7.3	carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)	824	0	MG	
			A48809	carboxylesterase - human	823	0	MG	
			BAA0465 0.1	carboxylesterase	823	0		
			AAC6063 1.2	acyl coenzyme A:cholesterol acyltransferase	822	0	MG	
			I61085	carboxylesterase - human	822	0	MG	
			BAB8565 6.1	brain carboxylesterase hBr2	822	0		
			AAD5317 5.1	egasyn	821	0	MG	
			P23141	Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)	821	0		
			NP_03625 4.1	carboxylesterase 3; brain carboxylesterase BR3	794	0	MG	
			I57004	carboxylesterase - human (fragment).	734	0	MG	
			CAA3714 7.1	serine esterase N-terminal truncated (503 AA)	731	0		
			AAA8393 2.1	carboxylesterase	631	1.00e -179	MG	
			BAA8499 5.1	brain carboxylesterase hBr1	594	1.00e -168	MG	
			NP_00386 0.1	carboxylesterase 2; intestinal carboxylesterase; liver carboxylesterase-2	463	1.00e -129	MG	
			AAH3209 5.1	Similar to carboxylesterase 2 (intestine, liver)	463	1.00e -129	MG	
			AAB0361 1.1	carboxylesterase hCE-2	462	1.00e -129	MG	
			CAD2853 1.1	hypothetical protein	449	1.00e -125	MG	

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			NP_05736 4.1	carboxylesterase-related protein	434	1.00e-120	MG	
AK01416 6 BAB2918 7.1	Mm.230 82	F:(C-D) -1.58	O76062	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1)	536	1.00e-169	MG	
			AAH1285 7.1	Similar to transmembrane 7 superfamily member 2	535	1.00e-169	MG	
			AAH0905 2.1	Similar to transmembrane 7 superfamily member 2	535	1.00e-169	MG	
			AAH3835 3.1	Similar to RIKEN cDNA 3110041O18 gene	469	1.00e-149	MG	
			NP_00326 4.1	transmembrane 7 superfamily member 2	514	1.00e-144	MG	
			XP_00179 5.5	similar to Lamin B receptor (Integral nuclear envelope inner membrane protein) (LMN2R)	411	1.00e-116	MG	
			AAA5949 5.1	integral nuclear envelope inner membrane protein	411	1.00e-116	MG	
			NP_00228 7.1	lamin B receptor	407	1.00e-115	MG	
AK00506 0 BAB237 84.1	Mm.291 25	F:(C-IR)-2.58 F:(C-D)-2.09	AAH22526					
			NP_112569	alanine-glyoxylate aminotransferase 2-like 1	858	0		
			NP_699204	hypothetical protein MGC45484	620	1.00e-177		
			NP_114106	alanine-glyoxylate aminotransferase 2	273	7.00e-73		
			NP_116310	hypothetical protein MGC15875	218	4.00e-56		
NM_01581 4 NP_05662 9.1	Mm.5514 3	F:(C-D)-2.18	BAA87044	Dickkopf-3	556	1.00e-158		
			NP_037385	dickkopf homolog 3; RIG-like 7-1; RIG-like 5-6	556	1.00e-158		
			IC7188	REIC protein	553	1.00e-157		
			AAB92664	RIG-like 7-1	301	6.00e-84		
			BAC03555	unnamed protein product	228	3.00e-59		
NM_02347 8 NP_07598 7.1	Mm.4621 4	F:(C-IR)-2.08	O75631	Uroplakin III precursor (UPIII)	496	1.00e-140		
			NP_00888 4	uroplakin 3	496	1.00e-140		
			BAA25678	uroplakin 3	439	1.00e-123		
NM_01028 9 NP_03441 9.1	Mm.4681 5	F:(C-D)-2.07	NP_115991	connexin 62	737	0		
			AAK55516	connexin 58	343	4.00e-94		



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			NP_110399	connexin 59; gap junction alpha 10	343	4.00e-9	4
			NP_005258	gap junction protein, alpha 8, 50kDa (connexin 50); gap junction membrane channel protein alpha-8; connexin 50; Gap junction membrane channel protein alpha-8 (connexin 50); gap junction protein, alpha 8, 50kD (connexin 50)	266	7.00e-7	1
			P48165	Gap junction alpha-8 protein (Connexin 50) (Cx50) (Lens fiber protein MP70).	265	1.00e-7	0
			NP_068773	gap junction protein, alpha 3, 46kDa (connexin 46); gap junction protein, alpha 3, 46kD (connexin 46)	265	1.00e-7	0
			Q9Y6H8	Gap junction alpha-3 protein (Connexin 46) (Cx46).	265	1.00e-7	0
			I38429	connexin40	251	2.00e-6	6
			NP_005257	gap junction protein, alpha 5, 40kDa (connexin 40); gap junction protein, alpha 5, 40kD (connexin 40)	249	5.00e-6	6
			P35212	Gap junction alpha-4 protein (Connexin 37) (Cx37).	246	5.00e-6	5
			AAD31871	connexin 37	246	5.00e-6	5
			AAD31873	connexin 37	246	5.00e-6	5
			AAD56533	truncated connexin 37 polymorph	246	5.00e-6	5
			AAD31872	connexin 37	243	4.00e-6	4
			NP_000156	connexin 43; gap junction protein, alpha 1, 43kD; oculodentodigital dysplasia (syndactyly type III)	243	4.00e-6	4
			AAD31870	connexin 37	243	5.00e-6	4
			NP_002051	connexin 37; gap junction protein, alpha 4, 37kD (connexin 37); gap junction protein, alpha 4, 37kD	238	2.00e-6	2
			NP_005488	gap junction protein, alpha 7, 45kDa (connexin 45); gap junction protein, alpha 7, 45kD (connexin 45)	233	7.00e-6	1
			NP_003995	gap junction protein, beta 2, 26kDa (connexin 26); gap junction protein, beta 2, 26kD (connexin 26)	204	3.00e-5	2
			AAF91440	gap junction protein beta 2	202	8.00e-5	2
			AAH35840	Similar to gap junction protein, alpha 12, 47kDa	196	5.00e-5	0
			NP_065168	connexin46.6	196	5.00e-5	0
			CAA54061				
			NP_005133	gastric intrinsic factor (vitamin B synthesis); Gastric intrinsic factor	676		0
					674		0
			NP_000505				
			AAD43139	glial cell derived neurotrophic factor precursor; glial cell line derived neurotrophic factor	345	3.00e-9	4
				glial cell line-derived neurotrophic	309	2.00e-8	3
			AAB33493	astrocyte-derived trophic factor 1, ATF-1 [human, caudate, Peptide, 185 aa].	292	2.00e-7	8
			NP_000763.1	cytochrome P450, family 2, subfamily C, polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; microsomal monooxygenase; flavoprotein-linked monooxygenase	629	1.00e-1	80

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		P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C).	627	1.00e-1 79
		NP_000760. 1	cytochrome P450, family 2, subfamily C, polypeptide 19; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	618	1.00e-1 77
		F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19	612	1.00e-1 75
		NP_000762. 2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	611	1.00e-1 75
		BAA00123. 1	cytochrome P-450	611	1.00e-1 75
		AAB23864. 2	cytochrome P-450	611	1.00e-1 75
		I506290A	cytochrome P450	610	1.00e-1 74
		P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP).	605	1.00e-1 73
		AAA52157. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	605	1.00e-1 73
		P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20)(P450 IIC2) (S-mephenytoin 4-hydroxylase).	600	1.00e-1 71
		AAH20596. 1	Unknown (protein for MGC:22146)	599	1.00e-1 71
		AAA52161. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	598	1.00e-1 71
		I52418	cytochrome P450 - human	598	1.00e-1 71
		NP_00076 1.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	597	1.00e-1 70
		AAB35292. 1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8[human, kidney, Peptide Partial, 485 aa].	596	1.00e-1 70
		AAA52160. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	595	1.00e-1 70
		G38462	cytochrome P450 2C17 - human	516	1.00e-1 46
		AAA52159. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	514	1.00e-1 45
		S21423	cytochrome P450 2C - human	497	1.00e-1 40
		NP_000764. 1	cytochrome P450, family 2, subfamily E, polypeptide 1; cytochrome P450, subfamily IIE (ethanol-inducible), polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)	478	1.00e-1 35
		AAD13753. 1	cytochrome P450 2E1	478	1.00e-1 35
		AAF13601. 1	cytochrome P450-2E1	478	1.00e-1 34
		NP_110518. 1	cytochrome P450, subfamily IIC, polypeptide 8 isoform 2; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	439	1.00e-1 23
		NP_000765. 2	cytochrome P450, family 2, subfamily F, polypeptide 1; cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	436	1.00e-1 22

			AAL69852. 1	cytochrome P450 2F1	430	1.00e-1 20
			NP_000757. 2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	427	1.00e-1 19
			Q16696	Cytochrome P450 2A13 (CYP11A13).	422	1.00e-1 18
			P24903	Cytochrome P450 2F1 (CYP11F1).	417	1.00e-1 16
5			NP_000753. 2	cytochrome P450, family 2, subfamily A, polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	417	1.00e-1 16
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6	416	1.00e-1 16
			NP_000755. 2	Cytochrome P450 2A7 (CYP11A7) (P450-IIA4).	415	1.00e-1 15
			P20853	Cytochrome P450 2A7 (CYP11A7) (P450-IIA4).	414	1.00e-1 15
			P11509	Cytochrome P450 2A6 (CYP11A6) (Coumarin 7-hydroxylase) (IIA3)(CYP2A3) (P450(I)).	414	1.00e-1 15
10			C34271	cytochrome P450 2A4 - human	413	1.00e-1 15
			NP_000758. 1	cytochrome P450, family 2, subfamily B, polypeptide 6; cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	413	1.00e-1 15
			AAF13600. 1	cytochrome P450-2A6	413	1.00e-1 15
			I609083A	cytochrome P450IIA	413	1.00e-1 15
			CAA32097. 1	cytochrome P-450IIA (AA 1 - 489)	413	1.00e-1 15
15			CAA32117. 1	P-450 IIA3 protein (1 is 3rd base in codon)	410	1.00e-1 14
			AAF13602. 1	cytochrome P450-2B6	410	1.00e-1 14
			I38967	cytochrome P450 - human	403	1.00e-1 12
			I38965	cytochrome P450 - human	399	1.00e-1 11
			I38966	cytochrome P450 - human	356	5.00e-9 8
20			NP_085079. 2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 2	348	1.00e-9 5
			NP_085125. 1	cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P450, subfamily IIS, polypeptide 1	342	1.00e-9 3
			BAB55227. 1	unnamed protein product	337	3.00e-9 2
			NP_00076 6.2	cytochrome P450, family 2, subfamily J, polypeptide 2; cytochrome P450, subfamily IJJ (arachidonic acid epoxidase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase	333	4.00e-9 1
			BAB5489. 1	cytochrome P450 2J2	333	6.00e-9 1
25			AAL31348. 1	S-mephenytoin 4-hydroxylase	319	7.00e-8 7
			CAA35915. 1	cytochrome P-450 HPH (120 AA)	308	4.00e-8 3
			AAD13466. 1	cytochrome P-450 2C	306	8.00e-8 3
			AAH25761. 1	Similar to hypothetical protein FLJ20359	300	5.00e-8 1
			AAA53500. 1	cytochrome P450 IID6	291	2.00e-7 8



Subtable 1B - Unfavorable

Main	Unigene	Behavior	Human Protein	Human Protein Name	Score	E-Value	BLASTx
5	NM_019634 NP_062608.1	U:(HI-D) 2.86	NP_004606.2	transmembrane 4 superfamily member 2; membrane component, x chromosome, surface marker 1; T-cell acute lymphoblastic leukemia associated antigen 1; transmembrane protein A15; tetraspanin protein; cell surface glycoprotein A15; CD231 antigen; transmembrane 4 superfamily 2b	497	1.0e-139	MG
			CAB65594.1	tetraspanin protein	486	1.0e-139	MG
			I39368	T-cell acute lymphoblastic leukemia associated antigen 1 - human	495	1.0e-139	MG
			AAH18036.1	Unknown (protein for MGC:26217)	494	1.0e-138	MG
			AAF44123.1	TALLA-1	450	1.0e-125	MG
10			NP_003261.1	transmembrane 4 superfamily member 6; tetraspanin TM4SF; A15 homolog; tetraspanin TM4-D; tetraspanin 6	295	1.0e-78	MG
			NM_016875 NP_058571.1	germ cell specific Y-box binding protein; contrin	285	1.0e-75	MG
			AAH33800.1		285	1.0e-75	MG
15	AF001293 AAB58795.1	U:(HI-D) 2.59	XP_012694.8	similar to zinc finger protein, subfamily 1A, 3 (Aiolos)	920	0	MG
			NP_036613.1	zinc finger protein, subfamily 1A, 3 (Aiolos)	911	0	MG
			CAC80429.1	AIOLOS isoform four	822	0	MG
			CAC80427.1	AIOLOS isoform two	753	0	MG
			CAC80428.1	AIOLOS isoform three	735	0	MG
20			CAC80431.1	AIOLOS isoform six	548	1.0e-145	MG
			CAC80430.1	AIOLOS isoform five	516	1.0e-145	MG
			NP_006051.1	zinc finger protein, subfamily 1A, 1 (Ikaro); Ikaro (zinc finger protein)	506	1.0e-142	MG
			AAB50683.1	hik1	493	1.0e-138	MG
			NP_057344.1	zinc finger protein, subfamily 1A, 2 (Helios); zinc finger DNA binding protein Helios	466	1.0e-130	MG
25			AAH18349.1	Unknown (protein for MGC:17055)	448	1.0e-124	MG
			AAH28936.1	Similar to zinc finger protein, subfamily 1A, 2 (Helios)	417	1.0e-115	MG
			BAB47411.1	KIAA1782 protein	406	1.0e-112	MG
			NP_071910.1	zinc finger protein, subfamily 1A, 4 (Eos); zinc finger transcription factor Eos	403	1.0e-111	MG
30							

5	NM_009895 NP_034025.1	Mm.4592	U:(HI-D) 2.45	NP_659508.1	cytokine-inducible SH2-containing protein isoform 2; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling	469	1.0e-131	MG	
				AAF97410.1	cytokine-inducible inhibitor of signaling type 1b	456	1.0e-127	MG	
				NP_037456.4	cytokine-inducible SH2-containing protein isoform 1; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling	456	1.0e-127	MG	
10	NM_018830 NP_061300.1	Mm.104900	U:(HI-D) 2.42	NP_063946.1	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2; N-acylsphingosine amidohydrolase 2; mitochondrial ceramidase; N-acylsphingosine amidohydrolase (acid ceramidase) 2	1219	0	MG	
	NM_008597 NP_032623.1	Mm.193459	U:(HI-D) 2.36	NP_000891.1	matrix Gla protein	167	7.0e-41	MG	
15	NM_009234 NP_033260.1	Mm.6238	U:(HI-D) 2.38	NP_003099.1	SRY (sex determining region Y)-box 11; SRY (sex-determining region Y)-box 11	415	1.0e-115	MG	
20	AF398969 AAK97491.1	Mm.200766	U:(HI-D) 2.35	NP_077000.1	ankyrin repeat and SOCS box-containing 8	552	1.0e-166	MG	
25	NM_016970 NP_058666.1	Mm.20434	U:(HI-D) 2.13	AAC32200.1	ITIM-containing receptor MAFA-L	223	6.0e-57	MG	
				NP_005801.2	killer cell lectin-like receptor subfamily G, member 1; mast cell function-associated antigen (ITIM-containing)	221	2.0e-56	MG	
				AAC34731.1	mast cell function-associated antigen	215	1.0e-54	MG	
30	NM_009344 NP_033370.1	Mm.3117	U:(HI-D) 2.1	NP_031376.1	pleckstrin homology-like domain, family A, member 1; PQ-rich protein	379	1.0e-104	MG	
				AAH18929.1	Similar to T-cell death associated gene	235	1.0e-60	MG	
35	NM_009964 NP_034094.1	Mm.178	U:(HI-D) 2.06	O43416	HEAT-SHOCK 20 KD LIKE-PROTEIN	337	1.0e-91	MG	
				NP_001876.1	crystallin, alpha B; crystallin, alpha-2; Rosenthal fiber component; heat-shock 20 kD like-protein	336	3.0e-91	MG	
40	NM_013565 NP_038593.1	Mm.57035	U:(HI-D) 2.05	NP_002195.1	integrin alpha 3 isoform a precursor	1778	0	MG	
				BAA00845.1	VLA-3 alpha subunit	1741	0	MG	
				P26006	Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c)	1723	0	MG	
45				NP_005492.1	integrin alpha 3 isoform b, precursor	1721	0	MG	
				CAA42099.1	integrin alpha6 subunit	587	1.0e-166	MG	
				NP_000201.1	Integrin alpha chain, alpha 6	582	1.0e-164	MG	

			AAD48469.1	Integrin alpha 6	582	1.0e-164	MG	
			B36429	integrin alpha-6 chain precursor, splice form A [validated]	578	1.0e-163	MG	
			CAB41534.1	Integrin alpha 7 chain	576	1.0e-163	MG	
			NP_002197.1	integrin alpha 7 precursor	575	1.0e-162	MG	
5			AAC18968.1	Integrin alpha 7	573	1.0e-162	MG	
			Q13683	Integrin alpha-7 precursor	561	1.0e-158	MG	
			A41543	Integrin alpha-6 chain precursor, splice form B	560	1.0e-158	MG	
			P23229	Integrin alpha-6 precursor (VLA-6) (CD49f)	557	1.0e-157	MG	
10	NM_013805 NP_038833.1	Mm.22768 U:(HI-D) 2.04	AAH19290.1	Unknown (protein for IMAGE:2822745)	320	4.0e-86	MG	
			NP_003268.1	transmembrane protein claudin 5; androgen withdrawal and apoptosis induced protein RVP1 (rat)-like; Claudin-5 (transmembrane protein deleted in velocardiofacial syndrome)	315	1.0e-84	MG	
15	AK014697 BAB29508.1	Mm.159563 U:(HI-D) 2.01	NP_110415.1	DC-specific transmembrane protein	525	1.0e-147	MG	
20	NM_009255 NP_033281.1	Mm.3093 U:(HI-D) 2.01	XP_059422.1	similar to tropomyosin, fibroblast - human	691	0	MG	
			P07093	Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease inhibitor 7)	684	0	MG	
			A26061	glia-derived neurite promoting factor precursor	682	0	MG	
			pdb 1DB2	Plasminogen Activator Inhibitor-1	310	4.0e-83	MG	
25			CAA28444.1	plasminogen activator inhibitor	310	4.0e-83	MG	
			pdb 1LJ5	Plasminogen Activator Inhibitor-1; Chain: A; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai	310	4.0e-83	MG	
			NP_000593.1	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1; plasminogen activator inhibitor, type 1	310	4.0e-83	MG	
			AAA60008.1	prebeta-migrating plasminogen activator inhibitor	310	4.0e-83	MG	
			AAA60009.1	plasminogen activator inhibitor 1	308	1.0e-82	MG	
30			pdb 9PA1	Cleaved Substrate Variant Of Plasminogen Activator Inhibitor-1	308	1.0e-82	MG	
			pdb 1A7C	Human Plasminogen Activator Inhibitor Type-1 In Complex With A Pentapeptide	308	2.0e-82	MG	
			pdb 1B3K	Plasminogen Activator Inhibitor-1	307	3.0e-82	MG	
			pdb 1DVM	Active Form Of Human Pai-1	305	2.0e-81	MG	
			CAA31208.1	PAI precursor polypeptide	305	2.0e-81	MG	
			NP_005016.1	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1; protease inhibitor 12 (neuroserpin)	243	7.0e-63	MG	

			AAH18043.1	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1	240	5.0e-62	MG	
			NP_006208.1	protease inhibitor 14; pancpin	218	1.0e-55	MG	
5	NM_017480 NP_059508.1	Mm.42044 U:(C-HI) 6.6	NP_036224.1	inducible T-cell co-stimulator; activation-inducible lymphocyte immunomediatory molecule; inducible costimulator	264	3.0e-69	MG	
			AAH28006.1	Similar to inducible T-cell co-stimulator	218	1.0e-54	MG	
10	NM_011704 NP_035834.1	Mm.27154 U (C-HI) 4.37, U (C-D) 3.14, U (HI-D) 2.37	NP_004657.1	vanin 1 precursor; Vannin 1; pantetheinase	795	0	MG	
			AAF21453.1	Tiff66	793	0	MG	
			CAB40075.1	dJ55C23.1 (vanin 1)	793	0	MG	
15			NP_060869.1	vanin 3 isoform 1 precursor; VNN3 protein; pantetheinase	657	0	MG	
			CAB40076.1	dJ55C23.2 (vanin 2)	639	0	MG	
			NP_004656.2	vanin 2, isoform 1 precursor; Vannin 2; pantetheinase	638	0	MG	
			CAA10569.1	VNN2 protein	635	0	MG	
			NP_511043.1	vanin 2, isoform 2; Vannin 2; pantetheinase	597	1.0e-169	MG	
20			P43251	Biotinidase precursor	382	1.0e-105	MG	
			NP_000051.1	biotinidase precursor	382	1.0e-105	MG	
			CAC33872.1	dJ55C23.5.1 (vanin 3, isoform 1)	342	1.0e-92	MG	
25	M12571 AAA57234.1	Mm.196559 U:(C-HI) 3.58	NP_005336.2	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1	635	0	MG	
			P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	635	0	MG	
			NP_005337.1	heat shock 70kDa protein 1B; heat shock 70kD protein 1B	633	1.0e-180	MG	
			A29160	dnaK-type molecular chaperone HSPA1L	628	1.0e-179	MG	
30			XP_175177.1	heat shock 70kD protein 1-like	588	1.0e-167	MG	
			BAA32521.1	Heat shock protein 70 testis variant	586	1.0e-166	MG	
			NP_005518.1	heat shock 70kDa protein 1-like; Heat-shock 70kD protein-like-1	586	1.0e-166	MG	
			XP_166348.1	similar to heat shock protein	586	1.0e-166	MG	
			AAH34483.1	heat shock 70kD protein 1-like	585	1.0e-166	MG	
35			NP_068814.2	heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2	567	1.0e-160	MG	
			AAH36107.1	Unknown (protein for MGC:33922)	587	1.0e-160	MG	
			NP_06588.1	Heat shock protein 70 testis variant	565	1.0e-160	MG	



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			AAH07276.1	Similar to heat shock cognate 71-kd protein	565	1.0e-160	MG	
			AAD11466.1	heat shock protein	564	1.0e-159	MG	
			AAH35665.1	heat shock 70kDa protein 6 (HSP70B')	555	1.0e-157	MG	
			NP_002146.1	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B'); Heat-shock 70kD protein-6 (HSP70B')	552	1.0e-156	MG	
	NM_007585 NP_031611.1	Mm.584 U:(C-HI) 3.49, U:(C-D) 4.83	NP_004030.1	annexin A2; annexin II; lipocortin II; Annexin II (lipocortin I); calpactin I, heavy polypeptide (p36); annexin II (lipocortin II); calpactin I, heavy polypeptide); annexin II (lipocortin II)	654	0	MG	
			AAH09564.1	annexin A2	653	0	MG	
			AAH23990.1	annexin A2	653	0	MG	
			CAB99342.1	bA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))	641	0	MG	
			NP_000691.1	annexin I; annexin I (lipocortin I); lipocortin I	335	8.0e-91	MG	
			pdb 1AIN	Annexin I	335	8.0e-91	MG	
			NP_001144.1	annexin IV; annexin IV (placental anticoagulant protein II); placental anticoagulant protein II	297	2.0e-79	MG	
			P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41)	297	2.0e-79	MG	
			AAC41689.1	protein PP4-X	297	2.0e-79	MG	
			NP_001148.1	annexin A11; annexin XI; autoantigen, 56-kD; calyculin-associated annexin 50	294	2.0e-78	MG	
			NP_004024.1	annexin VI isoform 2; annexin VI (p68); calcium-binding protein p68; calphobindin II;	291	2.0e-77	MG	
			CAA68286.1	protein p68 (1 - 673)	288	1.0e-76	MG	
			pdb 1M9I	Annexin Vi; Chain: A; Synonym: Lipocortin VI, P68, P70, Protein III, Chromobindin 20, 67 Kda Calelectrin, Calphobindin-II, Cpb- II	288	1.0e-76	MG	
			NP_001146.1	annexin VI isoform 1; annexin VI (p68); calcium-binding protein p68; calphobindin II; calelectrin F498	287	1.0e-76	MG	
			P08133	Annexin VI (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)	286	1.0e-76	MG	
			pdb 1AXN	Annexin III	281	1.0e-74	MG	
			NP_005130.1	annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calcimedlin 35-alpha); calcimedlin 35-alpha	281	1.0e-74	MG	
			pdb 1HVD	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutation With Glu 17 Replaced By Gly (E17G)	274	2.0e-72	MG	
			NP_001145.1	annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoagulant protein I	274	2.0e-72	MG	
			pdb 1ANW	Annexin V	274	2.0e-72	MG	

			pdj1HVF	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) Mutant With Glu 17 Replaced By Gly, Glu 78 Replaced By Gln (E17G, E78Q) Complexed With Calcium		4.0e-		
			AAH18671.1	annexin A5	273	72	MG	
			pdj1HVG	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutant With Glu 78 Replaced By Gln (E78Q) (Second Crystal Form)	273	72	MG	
			LUHU8	annexin VIII - human	273	72	MG	
5			NP_001621.1	annexin VIII; Annexin VII	271	71	MG	
			pdj1SAV	Annexin V; Chain: Null; Engineered: Yes; Mutation: P13, P87, P119, P163, and P248 Substituted With Thioproline (Prs); Biological_Unit: Monomer	271	71	MG	
			XP_036593.2	similar to annexin A8	271	71	MG	
			AAB46383.1	anexin VIII	265	69	MG	
10			NP_004025.1	annexin VII isoform 2; annexin VII (synexin); synexin	263	69	MG	
			NP_001147.1	annexin VII isoform 1; annexin VII (synexin); synexin	262	69	MG	
			XP_054475.4	similar to annexin A8	261	68	MG	
			CAC34622.1	annexin A13 isoform b	257	67	MG	
			NP_004297.1	annexin A13; annexin XIII; annexin, intestine-specific	252	66	MG	
15			AAH05830.1	Unknown (protein for MGC:1825)	248	64	MG	
			AAG16780.1	keratinocyte annexin-like protein	245	63	MG	
			NP_003559.1	annexin 31; annexin XXXI	245	63	MG	
20	NM_007980 NP_032006.1	Mm.28398 U:(C-HI) 3.49, U:(C-D) 2.22	NP_000125.1	Intestinal fatty acid binding protein 2; Fatty acid-binding protein, intestinal; I-FABP; fatty acid binding protein 2, intestinal	219	56	MG	
			pdj3IFB	Intestinal Fatty Acid Binding Protein; Chain: A; Synonym: I-Fabp	218	56	MG	
25	NM_007809 NP_031835.1	Mm.1262 U:(C-HI) 3.41, U:(C-D) 3.69	NP_000093.1	cytochrome P450, subfamily XVII polypeptide; steroid 17-alpha-monooxygenase; steroid 17-alpha-hydroxylase/17,20 lyase; cytochrome p450 XVIIA1	710	0	MG	
			AAA59984.1	cytochrome P450c17	709	0	MG	
			AAA52140.1	steroid 17-alpha-hydroxylase	708	0	MG	
30			CAA26458.1	cytochrome P(1)-450	248	64	MG	
			NP_000490.1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	248	64	MG	

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			AAA52139. 1	cytochrome P-450-1	248	9.0e-64	MG	
			AAK25728. 1	cytochrome P-450-1	231	2.0e-59	MG	
			NP_000752 .1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase	231	2.0e-59	MG	
			AAF13599. 1	cytochrome P450-1A2	230	4.0e-59	MG	
			AAA35738. 1	cytochrome P450 4	229	9.0e-59	MG	
			P08686	Cytochrome P450 XXIB (Steroid 21-hydroxylase) (P450-C21B)	228	2.0e-58	MG	
			AAA52063. 1	CYP21B protein	226	6.0e-58	MG	
			NP_000491 .2	cytochrome P450, subfamily XXIA, polypeptide 2; steroid 21-monooxygenase; steroid 21-hydroxylase	226	6.0e-58	MG	
			AAA52064. 1	21-hydroxylase B	226	6.0e-58	MG	
			AAA52065. 1	mutant 21-hydroxylase B	226	6.0e-58	MG	
			CAA41709. 1	steroid 21-monooxygenase	224	2.0e-57	MG	
			AAC50809. 1	cytochrome P450 CYP1B1	224	3.0e-57	MG	
			NP_000095 .1	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	224	3.0e-57	MG	
			AAB59440. 1	steroid 21-hydroxylase	224	3.0e-57	MG	
	AK007868 BAB25319. 1	Mm.23780 U:(C-HI) 3.19, U:(C-D) 2.42	NP_071733 .1	chromosome 11 open reading frame 24	229	1.0e-58	MG	
			AAH11765. 1	chromosome 11 open reading frame 24	229	1.0e-58	MG	
	U67189 AAB50619. 1	Mm.181709 U:(C-HI) 3.17	O15492	Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R) (A28-RGS14P)	323	2.0e-87	MG	
			NP_002919 .1	regulator of G-protein signaling 16; Regulator of G protein signaling-16	320	2.0e-86	MG	
	M63245 AAA91867. 1	Mm.19143 U:(C-HI) 3.05	NP_000679 .1	aminolevulinate, delta-, synthase 1	833	0	MG	
			CAA68506. 1	5-aminolevulinate synthase precursor	808	0	MG	
			CAB06076. 1	5-aminolevulinic acid synthase	645	0	MG	
			P22557	5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-E)	645	0	MG	
			CAA39795. 1	delta-aminolevulinate synthase (erythroid)	644	0	MG	
			NP_000023 .1	aminolevulinate, delta-, synthase 2; Aminolevulinate, delta-, synthase-2	644	0	MG	
			AAH30230. 1	Similar to aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	642	0	MG	

			AAG35538.1	PRO2399	350	3.0e-95	MG	
5	NM_007437 NP_031463.1	Mm.4210	U:(C-HI) 3.02	XP_045060.2	similar to fatty aldehyde dehydrogenase	751	0	MG
			NP_000373.1	aldehyde dehydrogenase 3A2; aldehyde dehydrogenase 10; aldehyde dehydrogenase 3 family, member A2; fatty aldehyde dehydrogenase	751	0	MG	
			NP_000682.3	aldehyde dehydrogenase 3 family, member A1; aldehyde dehydrogenase, dimeric NADP-preferring; acetaldehyde dehydrogenase; ALDH, stomach type	572	1.0e-162	MG	
			P30838	Aldehyde dehydrogenase, dimeric NADP-preferring (ALDH class 3) (ALDHIII)	572	1.0e-162	MG	
10			A42584	aldehyde dehydrogenase [NAD(P)] (EC 1.2.1.5) 3 -	572	1.0e-162	MG	
			AAH04370.1	aldehyde dehydrogenase 3	572	1.0e-162	MG	
			BAC04239.1	unnamed protein product	473	1.0e-132	MG	
			NP_000685.1	aldehyde dehydrogenase 3B1; aldehyde dehydrogenase 7; aldehyde dehydrogenase 3 family, member B1	453	1.0e-126	MG	
			AAH33099.1	Similar to aldehyde dehydrogenase 3 family, member B1	431	1.0e-119	MG	
			NP_000686.1	aldehyde dehydrogenase 3B2; aldehyde dehydrogenase 8; aldehyde dehydrogenase 3 family, member B2	392	1.0e-107	MG	
15			AAH07685.1	Similar to aldehyde dehydrogenase 3 family, member B2	391	1.0e-107	MG	
			BAC03897.1	unnamed protein product	390	1.0e-107	MG	
20	NM_022331 NP_071726.1	Mm.29151	U:(C-HI) 3.00, U:(C-D) 2.29	NP_055500.1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene	592	1.0e-168	MG
			AAC09357.1	unknown	525	1.0e-147	MG	
			AAG17233.1	unknown	295	2.0e-78	MG	
			AAH09739.1	Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	218	2.0e-55	MG	
25			NP_071768.2	hypothetical protein FLJ22313	216	1.0e-54	MG	
30	NM_007468 NP_031494.1	Mm.4533	U (C-HI) 2.98, U (C-D) 2.42, U (HI-D) 2.16	P06727	Apolipoprotein A-IV precursor (Apo-AIV)	432	1.0e-120	MG
			CAA31955.1	apolipoprotein A-IV precursor	431	1.0e-119	MG	
			NP_000473.1	apolipoprotein A-IV precursor	428	1.0e-119	MG	
			LPHUA4	apolipoprotein A-IV precursor [validated]	426	1.0e-118	MG	
			AAA51748.1	apolipoprotein A-IV precursor	422	1.0e-117	MG	
			AAB59516.1	apolipoprotein A-IV	277	2.0e-73	MG	

5	NM_00783 7 NP_031863. 1	Mm.7549	U:(C-HI) 2.98, U:(C-D) 2.16	AAB27103. 1	TLS-CHOP	245	5.0e- 64	MG	
				CAA63088. 1	chimeric cDNA from Myxoid liposarcoma	244	1.0e- 63	MG	
				NP_004074 .2	DNA-damage-inducible transcript 3; C/EBP homologous protein; growth arrest- and DNA damage-inducible	220	1.0e- 56	MG	
				JC1169	DNA-damage-inducible protein GADD153 - human	216	3.0e- 55	MG	
10	NM_00786 0 NP_031886. 1	Mm.2774	U:(C-HI) 2.84, U:(C-D) 2.06	P49895	Type I iodothyronine deiodinase (Type-I 5'deiodinase) (DIO1) (Type 1 DI) (5DI)	417	1.0e- 115	MG	
				NP_000783 .2	thyroxine deiodinase type 1; 5DI; thyroxine deiodinase type I (selenoprotein)	409	1.0e- 113	MG	
				AAH17955. 1	Similar to deiodinase, iodothyronine, type I	207	4.0e- 52	MG	
15	NM_01697 4 NP_058670. 1	Mm.3459	U (C-HI) 2.79, U (C-D) 4.24, U (HI-D) 2.47	Q10586	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)	399	1.0e- 110	MG	
				NP_001343 .1	D site of albumin promoter (albumin D-box) binding protein; D site of albumin promoter binding protein	399	1.0e- 110	MG	
				BAA05833. 1	TAXREB302	299	9.0e- 80	MG	
20				NP_002117 .1	hepatic leukemia factor	203	5.0e- 51	MG	
				Q10587	Thyrotroph embryonic factor	201	2.0e- 50	MG	
				B55558	thyrotroph embryonic factor - human	201	2.0e- 50	MG	
25				CAB62497. 1	dJ979N1.5 (thyrotrophic embryonic factor (ortholog of chicken vitellogenin gene-binding protein VBP beta/beta isoform) (isoform 2))	201	2.0e- 50	MG	
				NP_003207 .1	thyrotrophic embryonic factor; Thyrotroph embryonic factor	101	3.0e- 20	MG	
	AK007378 BAB24997. 1	Mm.35083	U:(C-HI) 2.77	NP_077016 .1	hypothetical protein MGC4504	379	e-104	MG	
30	NM_01137 5 NP_035505. 1	Mm.38248	U:(C-HI) 2.65, U:(C-D) 2.16	NP_003887 .1	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase); ganglioside G(M3) Synthase	628	1.0e- 179	MG	
				AAD14634. 1	CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase	628	1.0e- 178	MG	
				NP_006270 .1	sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase)	213	2.0e- 53	MG	
35				AAL14347. 1	Gal beta 1,3(4) GlcNAc alpha 2,3-sialyltransferase	202	2.0e- 50	MG	
	NM_00776 0 NP_031786. 1	Mm.20396	U:(C-HI) 2.57, U:(C-D) 2.16	NP_000746 .2	carnitine acetyltransferase precursor, Isoform 1	1151	0	MG	
				P43155	Carnitine O-acetyltransferase (Carnitine acetylase) (CAT)	1139	0	MG	
40				CAA55359. 1	carnitine acetyltransferase	1124	0	MG	
				NP_003994 .2	carnitine acetyltransferase Isoform 2	1117	0	MG	

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			NP_659006 .1	carnitine acetyltransferase precursor, isoform 3	514	1.0e-144	MG	
			P28329	Choline O-acetyltransferase (CHOACTase) (Choline acetylase) (ChAT)	470	1.0e-131	MG	
			AAK08951. 1	choline acetyltransferase isoform S	470	1.0e-131	MG	
			NP_065574 .1	choline acetyltransferase isoform 2; acetyl CoA:choline O-acetyltransferase	468	1.0e-130	MG	
			AAK08952. 1	choline acetyltransferase isoform R	468	1.0e-130	MG	
			NP_066266 .1	choline acetyltransferase isoform 1; acetyl CoA:choline O-acetyltransferase	465	1.0e-129	MG	
			T01786	choline acetyltransferase - human (fragment).	409	1.0e-113	MG	
NM_02057 0	Mm.143767	U:(C-HI) 2.55	NP_005422 .1	X-ray repair cross complementing protein 2; X-ray repair, complementing defective, repair in Chinese hamster; DNA repair protein XRCC2	422	1.0e-117	MG	
NM_01942 3	Mm.2567	U:(C-HI) 2.53, U:(C-D) 2.08	NP_060240 .1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	554	1.0e-156	MG	
NP_062296. 1			CAB89418. 1	dJ483K16.1.1 (novel protein (isoform 1))	369	1.0e-100	MG	
			NP_068586 .1	homolog of yeast long chain polyunsaturated fatty acid elongation	367	1.0e-100	MG	
			NP_073563 .1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4; Stargardt disease 3 (autosomal dominant)	262	3.0e-69	MG	
			CAC19496. 1	dJ92C4.1 (novel protein, partly predicted by Fgenesh and Genscan)	259	1.0e-87	MG	
NM_01997 7	Mm.158200	U:(C-HI) 2.51	AAF25204. 1	unknown	540	1.0e-152	MG	
NP_064361. 1			NP_060054 .2	aldehyde reductase (aldose reductase) like 6; similar to mouse aldehyde reductase 6 (renal); myo-inositol oxygenase; kidney-specific protein 32	535	1.0e-151	MG	
			AAK00766. 1	kidney-specific protein 32	528	1.0e-149	MG	
NM_03116 2	Mm.1224	U:(C-HI) 2.49	AAH25703. 1	CD3Z antigen, zeta polypeptide (TIT3 complex)	233	3.0e-60	MG	
NP_112439. 1			P20963	T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain)	228	2.0e-58	MG	
			NP_000725 .1	T-cell receptor zeta chain precursor	227	3.0e-58	MG	
			AAF34793. 1	T-cell receptor zeta chain precursor	213	4.0e-54	MG	
NM_01969 9	Mm.38901	U:(C-HI) 2.46	NP_004256 .1	fatty acid desaturase 2; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2	842	0	MG	
NP_062673. 1			AAH09011. 1	fatty acid desaturase 2	726	0	MG	
			AAG43192. 1	p5327	717	0	MG	
			T08765	probable delta-6 fatty acid desaturase (EC 1.14.99.-) - human (fragment).	605	1.0e-172	MG	

			NP_068373.1	fatty acid desaturase 3; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 3	598	1.0e+170	MG	
			BAC11182.1	unnamed protein product	575	1.0e-163	MG	
			BAB55103.1	unnamed protein product	575	1.0e-163	MG	
5			NP_037534.2	fatty acid desaturase 1; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5 desaturase; delta-5 fatty acid desaturase	575	1.0e-163	MG	
			AAH07846.1	fatty acid desaturase 1	572	1.0e-162	MG	
			AAF70457.1	delta-5 fatty acid desaturase	572	1.0e-162	MG	
			BAC11229.1	unnamed protein product	570	1.0e-161	MG	
			AAF29378.1	delta-5 desaturase	570	1.0e-161	MG	
			BAB55173.1	unnamed protein product	569	1.0e-161	MG	
10			AAC23396.1	BC269730_1	315	1.0e-108	MG	
			BAB55167.1	unnamed protein product	327	3.0e-88	MG	
15	NM_023719 NP_076208.1	Mm.77432 U:(C-HI) 2.36, U:(C-D) 2.42	BAB18859.1	VDUP1	761	0	MG	
			NP_006463.2	thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3	760	0	MG	
			XP_041721.2	similar to RIKEN cDNA 2410003C09 gene	326	1.0e-87	MG	
			AAH28704.1	Unknown (protein for IMAGE:4838787)	326	1.0e-87	MG	
20			BAA92614.1	KIAA1376 protein	308	8.0e-82	MG	
			XP_033042.2	similar to hypothetical protein CLONE24945	304	5.0e-81	MG	
			NP_056498.1	hypothetical protein CLONE24945	258	2.0e-66	MG	
			AAH22516.1	Unknown (protein for MGC:26574)	254	5.0e-66	MG	
			AAD20053.1	Unknown	214	7.0e-54	MG	
25	NM_013760 NP_038788.1	Mm.27432 U:(C-HI) 2.34, U:(C-D) 2.1	NP_036460.1	DnaJ (Hsp40) homolog, subfamily B, member 9; microvascular endothelial differentiation gene 1; DKFZP584F1862 protein; endoplasmic reticulum DnaJ homolog 4	391	1.0e-107	MG	
			AAD08848.1	similar to putative microvascular endothelial differentiation gene 1; similar to X98993 (PID:g1771560)	298	2.0e-79	MG	
30	NM_023184 NP_075673.1	Mm.41389 U:(C-HI) 2.34	NP_054798.1	Kruppel-like factor 15; KLF protein; kidney-enriched Kruppel-like factor	624	1.0e-178	MG	
35	NM_018791 NP_061261.1	Mm.103750 U:(C-HI) 2.32	NP_004225.2	zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)	919	0	MG	
			AAF88107.1	Hypothetical zinc finger-like protein	600	1e-17	MG	

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			AAF88103.1	zinc finger protein 226	588	1.0e-166	MG	
			Q9NYT6	Zinc finger protein 226	587	1.0e-166	MG	
			NP_057528.1	zinc finger protein 226; Kruppel-associated box protein	586	1.0e-166	MG	
			AAF63030.1	Zinc finger protein ZNF45	576	1.0e-163	MG	
			NP_003416.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain	573	1.0e-162	MG	
			XP_091906.2	similar to Zinc finger protein 229	548	1.0e-155	MG	
			AAD12728.1	zinc finger protein	541	1.0e-152	MG	
			AAF76875.1	zinc finger protein	533	1.0e-150	MG	
			NP_037530.1	zinc finger protein 224	518	1.0e-146	MG	
			NP_037512.1	zinc finger protein 228	517	1.0e-145	MG	
			XP_009363.3	similar to ZNF228 protein	515	1.0e-145	MG	
			AAG23968.1	ZNF228 protein	515	1.0e-145	MG	
			AAF88104.1	ZNF234	512	1.0e-144	MG	
			XP_044207.1	similar to Zinc finger protein 234 (Zinc finger protein HZF4)	512	1.0e-144	MG	
			I37570	zinc finger protein - human (fragment)	511	1.0e-143	MG	
			Q14588	Zinc finger protein 234 (Zinc finger protein HZF4)	511	1.0e-143	MG	
			AAF24967.1	ZNF225	507	1.0e-142	MG	
			NP_653290.2	hypothetical protein FLJ32191	501	1.0e-140	MG	
			NP_037494.1	zinc finger protein 225	501	1.0e-140	MG	
	AK007864 BAB25316.1	Mm.27338	U:(C-HI) 2.31	XP_084735.2	similar to RIKEN cDNA 1810054O13	384	1.0e-105	MG
				AAH17073	Similar to RIKEN cDNA 1810054O13 gene	346	7.0e-94	MG
	NM_019545 NP_062418.1	Mm.20413	U:(C-HI) 2.31	NP_057612.1	hydroxyacid oxidase 3; medium-chain 2-hydroxy acid oxidase HAOX3; (S)-2-hydroxy-acid oxidase; glycolate oxidase	645	0	MG
				NP_057611.1	hydroxyacid oxidase 2; long-chain L-2-hydroxy acid oxidase; (S)-2-hydroxy-acid oxidase; glycolate oxidase	474	1.0e-132	MG
				AAF14000.1	long-chain L-2-hydroxy acid oxidase	461	1.0e-128	MG
				NP_060015.1	hydroxyacid oxidase 1; (S)-2-hydroxy-acid oxidase; glycolate oxidase	300	3.0e-80	MG
				BAA82872.1	a liver-specific gene similar to the plant glycolate oxidase	299	8.0e-80	MG
	NM_011058 NP_035188.1	Mm.2924	U:(C-HI) 2.3	NP_006197.1	platelet-derived growth factor receptor alpha precursor	1905	0	MG



			NP_002600.1	platelet-derived growth factor receptor beta precursor; beta platelet-derived growth factor receptor	826	0	MG	
			AAA36427.1	platelet-derived growth factor receptor	825	0	MG	
			AAH32224.1	platelet-derived growth factor receptor, beta polypeptide	825	0	MG	
			AAC50969.1	KIT protein	523	1.0e-146	MG	
			NP_000213.1	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor	523	1.0e-146	MG	
			NP_005202.1	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	485	1.0e-135	MG	
			P07333	Macrophage colony stimulating factor 1 receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen)	485	1.0e-135	MG	
			CAA81393.1	FLT3 receptor tyrosine kinase	414	1.0e-113	MG	
			NP_004110.1	fms-related tyrosine kinase 3	411	1.0e-113	MG	
			A36873	protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human	405	1.0e-111	MG	
			AAH15186.1	Unknown (protein for MGC:14518)	363	2.0e-98	MG	
			AAC16449.1	vascular endothelial growth factor receptor	352	3.0e-95	MG	
			NP_002010.1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	352	3.0e-95	MG	
			NP_002011.1	fms-related tyrosine kinase 4; fms-related tyrosine kinase-4 (vascular endothelial growth factor receptor 3)	344	1.0e-92	MG	
			CAA48290.1	FTL4	343	2.0e-92	MG	
			P35916	Vascular endothelial growth factor receptor 3 precursor (VEGFR-3) (Tyrosine-protein kinase receptor FLT4)	343	2.0e-92	MG	
			AAC16450.1	vascular endothelial growth factor receptor 2	341	7.0e-92	MG	
			NP_002244.1	kinase insert domain receptor (a type III receptor tyrosine kinase); Kinase insert domain receptor	341	7.0e-92	MG	
			JC1402	protein-tyrosine kinase (EC 2.7.1.112) KDR - human	340	1.0e-91	MG	
			I58357	receptor tyrosine kinase - human (fragment).	340	1.0e-91	MG	
NM_010565	Mm.2594	U:(C-HI) 2.28	NP_005529.1	inhibin beta C chain preproprotein; activin beta-C chain	503	1.0e+141	MG	
NP_034695.1			NP_113667.1	activin beta E	207	1.0e-52	MG	
NM_011994	Mm.4817	U:(C-HI) 2.27	JC5712	adrenoleukodystrophy related protein	1353	0	MG	
NP_036124.1			NP_005155.1	ATP-binding cassette, sub-family D, member 2; adrenoleukodystrophy-like 1; hALDR	1348	0	MG	
			NP_000024.2	ATP-binding cassette, sub-family D (ALD), member 1; adrenoleukodystrophy protein	926	0	MG	
			I908394A	adrenoleukodystrophy protein	925	0	MG	
			P33897	Adrenoleukodystrophy protein (ALDP)	925	0	MG	

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			AAB27045.1	70-kd peroxisomal membrane protein homolog (internal fragment) [human, Peptide Partial, 388 aa]	549	1.0e-155	MG	
			AAB00541.1	adrenoleukodystrophy related protein	510	1.0e-143	MG	
			NP_002849.1	ATP-binding cassette, sub-family D, member 3; Peroxisomal membrane protein-1 (70kD); peroxisomal membrane protein 1 (70kD, Zellweger syndrome); peroxisomal membrane protein-1	448	1.0e-124	MG	
			S20313	peroxisomal membrane protein, 70K - human	448	1.0e-124	MG	
			CAA58470.1	70kD peroxisomal integral membrane protein	406	1.0e-112	MG	
NM_018817 NP_061287.1	Mm.36676	U:(C-HI) 2.27	NP_054859.2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1; HepA-related protein; SMARCA-like protein 1	1213	0	MG	
			AAH16482.1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	1210	0	MG	
			AAF24984.1	HepA-related protein HARP	1205	0	MG	
			T34557	hypothetical protein DKFZp434B1050.1 - human (fragment)	1125	0	MG	
			BAA90955.1	unnamed protein product	975	0	MG	
			BAC04536.1	unnamed protein product	220	1.0e-55	MG	
AK006096 BAB24407.1	Mm.38305	U:(C-HI) 2.24	AAH11587.1	Similar to RIKEN cDNA 1700018O18 gene	779	0	MG	
			BAC04100.1	unnamed protein product	770	0	MG	
			AAH06353.1	Similar to RIKEN cDNA 1700018O18 gene	550	1.0e-155	MG	
			XP_065744.2	similar to F16H11.1.p	286	8.0e-78	MG	
NM_019682 NP_062656.1	Mm.29908	U:(C-HI) 2.24	NP_003737.1	dynein, cytoplasmic, light polypeptide; Dynein, cytoplasmic, light chain (protein inhibitor of neuronal NOS); protein inhibitor of neuronal nitric oxide synthase	188	3.0e-47	MG	
NM_009154 NP_033180.1	Mm.24733	U:(C-HI) 2.23	NP_003957.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, 5A	1993	0	MG	
			BAA95969.1	KIAA1445 protein	1243	0	MG	
			XP_032249.3	similar to KIAA1445 protein	1243	0	MG	
			AAC14668.1	semaphorin F	949	0	MG	
AK005274 BAB23924.1	Mm.195961	U:(C-HI) 2.22, U:(C-D) 2.15	NP_115680.1	hypothetical protein MGC2605	471	1.0e-131	MG	
			AAK61250.1	similar to HAGH	376	1.0e-103	MG	

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			NP_005317.1	hydroxyacyl glutathione hydrolase; hydroxyacyl glutathione hydrolase; glyoxalase 2; Hydroxyacyl glutathione hydrolase; glyoxalase II; hydroxyacylglutathione hydroxylase	266	6.0e-70	MG	
			BAB70814.1	unnamed protein product	237	2.0e-69	MG	
NM_009315 NP_033341.1	Mm.1994	U:(C-HI) 2.2	NP_005632.1	TBP-associated factor 6 isoform alpha; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	979	0	MG	
			NP_620834.1	TBP-associated factor 6 isoform gamma; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	957	0	MG	
			NP_620835.1	TBP-associated factor 6 isoform delta; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	952	0	MG	
NM_011361 NP_035491.1	Mm.28405	U:(C-HI) 2.2	AAD41091.1	serine/threonine protein kinase sgk	797	0	MG	
			NP_005618.1	serum/glucocorticoid regulated kinase	796	0	MG	
			AAH15326.1	Unknown (protein for MGC:21163)	532	1.0e-149	MG	
			AAF12758.1	protein kinase	532	1.0e-149	MG	
			NP_037389.2	serum/glucocorticoid regulated kinase-like; cytokine-independent survival kinase	527	1.0e-148	MG	
			AAF12757.2	protein kinase	506	1.0e-142	MG	
			NP_057360.2	serum/glucocorticoid regulated kinase 2 isoform beta	506	1.0e-142	MG	
			NP_005456.1	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B	327	4.0e-88	MG	
NM_011844 NP_035974.1	Mm.194795	U:(C-HI) 2.19	NP_009214.1	monoglyceride lipase; lysophospholipase-like; likely ortholog of mouse monoglyceride lipase	538	1.0e-151	MG	
			CAC43316.1	monoglyceride lipase	528	1.0e-148	MG	
NM_018861 NP_061349.1	Mm.6379	U:(C-HI) 2.18	AAA19438.1	neutral amino acid transporter	676	0	MG	
			NP_003029.2	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; Solute carrier family 1 (glutamate/neutral amino acid transporter),	678	0	MG	
			I55389	neutral amino acid transporter - human	673	0	MG	
			BAA94861.1	hASCT1	670	0	MG	
			A47131	Na <sup>+</sup> -dependent neutral amino acid transporter SATT	630	1.0e-179	MG	

			NP_005619.1	solute carrier family 1 (neutral amino acid transporter), member 5; baboon M7 virus receptor; RD114 virus receptor; neutral amino acid transporter B	365	2.0e-99	MG	
			AAD09814.1	neutral amino acid transporter	365	2.0e-99	MG	
			AAH00062.1	solute carrier family 1 (neutral amino acid transporter), member 5	365	2.0e-99	MG	
			AAK77026.1	sodium-dependent neutral amino acid transporter type 2 truncated isoform	365	2.0e-99	MG	
			AAC50629.1	neutral amino acid transporter B	365	3.0e-99	MG	
			AAD09812.1	RD114/simian type D retrovirus receptor	381	5.0e-98	MG	
5			AF213258 AAQ43836	Mm.149760 U:(C-HI) 2.17, U:(C-D) 2.34 NP_690864.1	1995	0	MG	
				XP_032749.2	similar to membrane-associated guanylate kinase MAGI3	1989	0	MG
10				AAG24545.1	membrane-associated guanylate kinase MAGI3	1972	0	MG
				BAB13460.1	KIAA1634 protein	1590	0	MG
				CAC17586.1	dJ730K3.2 (similar to BAI1-associated protein)	1163	0	MG
				NP_038433.1	atrophin-1 interacting protein 1; activin receptor interacting p; KIAA0705 gene product	969	0	MG
				AAK94066.1	MAGI-1C beta	853	0	MG
15				AAK94064.1	MAGI-1B alpha beta	847	0	MG
				NP_004733.1	BAI1-associated protein 1; WW domain-containing protein 3	843	0	MG
				JE0209	brain-specific angiogenesis inhibitor-associated protein 1 - human	839	0	MG
				BAA31680.1	KIAA0705 protein	827	0	MG
				AAK94065.1	MAGI-1A	689	0	MG
20				CAC36032.1	bA473L1.1 (novel protein similar to BAI1-associated protein 1 (BAIAP1))	587	1.0e-166	MG
				BAB15479.1	unnamed protein product	300	1.0e-162	MG
				AAC04844.1	membrane associated guanylate kinase 1	450	1.0e-125	MG
			NM_008382 NP_032408.1	Mm.3510 U:(C-HI) 2.13 NP_113667.1		1.0e-151	MG	
25				NP_005529.1	inhibin beta C chain preproprotein; activin beta-C chain	243	1.0e-62	MG
			NM_011579 NP_035709.1	Mm.15793 U:(C-HI) 2.13 NP_062558.1		4.0e-60	MG	
30				NP_005186.1	CCAAT/enhancer binding protein (C/EBP), delta	343	3.0e-93	MG
			NM_007679 NP_031705.1	Mm.4639 U:(C-HI) 2.11		4.0e-92	MG	
35				A40225	transcription activator NF-IL6 beta - human	340		MG

			XP_171180 .1	similar to CCAAT/enhancer binding protein delta (C/EBP delta) (Nuclear factor NF-IL6-beta) (NF-IL6-beta)	340	4.0e- 92	MG	
5	NM_03088 7 NP_112149. 1	Mm.103560	U:(C-HI) 2.07 NP_569736 .1	Jun dimerization protein	244	3.0e+ 63	MG	
10	NM_00936 6 NP_033392. 1	Mm.20927	U:(C-HI) 2.06, U:(C-D) 2.89, U:(HI-D) 2.64 NP_006013 .1	transforming growth factor beta-stimulated protein TSC-22	213	7.0e- 54	MG	
			BAB46917. 1	cerebral protein-2	211	2.0e- 53	MG	
15	NM_01999 2 NP_064376. 1	Mm.38392	U:(C-HI) 2.06, U:(C-D) 2.23, U:(HI-D) 2.12 NP_036240 .1	BCR downstream signaling 1	465	1.0e- 130	MG	
20	NM_01941 5 NP_062288. 1	Mm.182905	U:(C-HI) 2.06 P55017	Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter) (Na-Cl symporter)	1795	0	MG	
			G01202	NaCl electroneutral Thiazide-sensitive cotransporter	1792	0	MG	
			NP_000330 .1	solute carrier family 12 (sodium/chloride transporters), member 3; Solute carrier family 12 (sodium/potassium/chloride transporters),	1792	0	MG	
			NP_001037 .1	solute carrier family 12 (sodium/potassium/chloride transporters), member 2; Solute carrier family 12 (sodium/potassium/chloride transporters),	1023	0	MG	
			NP_000329 .1	sodium potassium chloride cotransporter 2; Solute carrier family 12 (sodium/potassium/chloride transporters),	1022	0	MG	
			AAH33003. 1	lar to solute carrier family 12 (sodium/potassium/chloride transporters), member 2	944	0	MG	
25			PC4180	thiazide-sensitive sodium-chloride cotransporter - human (fragment)	662	0	MG	
			NP_006589 .1	solute carrier family 12 (potassium/chloride transporters), member 7; potassium/chloride transporter KCC4	316	1.0e- 84	MG	
			AAL32454. 1	sodium-potassium-chloride cotransporter	296	1.0e- 78	MG	
			BAA86490. 1	KIAA1176 protein	271	4.0e- 71	MG	
			AAG43493. 1	electroneutral potassium-chloride cotransporter KCC2	271	4.0e- 71	MG	
			NP_065759 .1	solute carrier family 12, (potassium-chloride transporter) member 5	271	4.0e- 71	MG	
30	AK002693 BAB22288. 1	Mm.41325	U:(C-HI) 2.04 NP_477513 .1	diacylglycerol O-acyltransferase 2 like 1; diacylglycerol acyltransferase 2-like	516	1.0e- 145	MG	
			CAD38961. 1	hypothetical protein	311	1.0e- 83	MG	
			AAH15234. 1	Unknown (protein for MGC:17881)	311	1.0e- 83	MG	
35			NP_115953 .1	diacylglycerol O-acyltransferase homolog 2; GS1999full	286	4.0e- 76	MG	
			CAD13492. 1	bA351K23.5 (novel protein)	258	1.0e- 67	MG	

			NP_079374 .1	hypothetical protein FLJ22644	241	1.0e-62	MG	
			AAD45832. 1	similar to predicted proteins AAB54240 (PID:g2088822) and S67138 (PID:g2132925)	208	1.0e-52	MG	
5	AK003722 BAB22959. 1	Mm.89830	U:(C-HI) 2.04 NP_008950 .1	ubiquitin-conjugating enzyme E2C; ubiquitin carrier protein E2-C	343	1.0e-93	MG	
			pdh117K	Ubiquitin-Conjugating Enzyme E2 H10; Chain: A, B; Synonym: Ubiquitin-Conjugating Enzyme Ubch10; Ec: 6.3.2.19;	340	2.0e-92	MG	
			CAC36108. 1	dJ447F3.2.4 (ubiquitin-conjugating enzyme E2 H10 (isoform 4))	285	8.0e-76	MG	
10	NM_01051 6 NP_034646. 1	Mm.1231	U:(C-HI) 2.04 AAG59863. 1	CYR61 protein	650	0	MG	
			O00622	CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (GIG1 protein)	648	0	MG	
			CAA72167. 1	CYR61 protein	648	0	MG	
15			NP_001545 .1	cysteine-rich, angiogenic inducer, 61; cysteine-rich heparin-binding protein 61; cysteine-rich, angiogenic inducer, 61	645	0	MG	
			AAF21597. 1	tumor RMS cell line RD specific product	486	1.0e-136	MG	
			CAC44023. 1	bA6918.1 (connective tissue growth factor)	330	5.0e-89	MG	
			NP_001892 .1	connective tissue growth factor	330	5.0e-89	MG	
			AAH15028. 1	nephroblastoma overexpressed gene	281	2.0e-74	MG	
20			NP_002505 .1	nov precursor	281	2.0e-74	MG	
			AAA75378. 1	connective tissue growth factor	268	3.0e-70	MG	
			NP_003873 .1	WNT1 inducible signaling pathway protein 1, isoform 1 precursor; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1; wnt-1 signaling pathway protein 1; connective tissue growth factor related protein WISP-1; Wnt-1 induced secreted protein 1	266	8.0e-70	MG	
			NP_569080 .1	WNT1 inducible signaling pathway protein 3, isoform 2; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3	216	7.0e-55	MG	
			NP_003871 .1	WNT1 inducible signaling pathway protein 3, isoform 1; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3	211	2.0e-53	MG	
25	NM_01035 4 NP_034484. 1	Mm.21109	U:(C-HI) 2.03 NP_000168 .1	gelsolin (amyloidosis, Finnish type); Gelsolin	1422	0	MG	
			Q9Y6U3	Adseverin (Scinderin)	904	0	MG	
			BAC11416. 1	unnamed protein product	904	0	MG	

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			AAK60494.1	scinderin	899	0	MG	
			NP_009058.1	villin 1; Villin-1	672	0	MG	
			AAD15423.1	similar to mouse adseverin(D5); similar to PID:g2218019	666	0	MG	
			BAB67798.1	KIAA1905 protein	666	0	MG	
			pdbj1DB0	Carboxy-Terminal Half Of Gelsolin (G4-G6) Bound To Actin	643	0	MG	
			NP_006567.2	advillin	640	0	MG	
			O75366	Advillin (p92)	638	0	MG	
			NP_149119.1	scinderin; adseverin; KIAA1905 protein	588	1.0e-167	MG	
			AAH17491.1	Similar to gelsolin (amyloidosis, Finnish type)	542	1.0e-153	MG	
			BAC11465.1	unnamed protein product	497	1.0e-139	MG	
			AAH04134.1	Similar to advillin	484	1.0e-129	MG	
			pdbj1JHW	Macrophage Capping Protein; Chain: A; Synonym: Actin-Regulatory Protein Cap-G; Engineered	389	1.0e-106	MG	
AK002717 XP_134867	Mm.46241	U:(C-HI) 2.02	NP_005692.1	RNA, U transporter 1; snurportin-1; snuportin-1	424	1.0e-169	MG	
AK004600 BAB23401.1	Mm.34514	U:(C-HI) 2.02	NP_062455.1	Rho guanine nucleotide exchange factor 3; RhoGEF protein; 59.8 kDA protein	941	0	MG	
			BAB14891.1	unnamed protein product	782	0	MG	
			AAH22249.1	Similar to Rho guanine nucleotide exchange factor (GEF) 3	590	1.0e-167	MG	
			CAA08974.1	guanine nucleotide-exchange factor	553	1.0e-156	MG	
			NP_003015.1	intersectin 1 (SH3 domain protein); Intersectin (SH3 domain protein 1A); SH3 domain protein-1A; human intersectin-SH3 domain-containing protein SH3P17	553	1.0e-156	MG	
			G01210	guanine nucleotide regulatory protein	500	1.0e-140	MG	
M62766 AAA37819.1	Mm.2226	U:(C-HI) 2.02	NP_000850.1	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	432	1.0e-120	MG	
			pdbj1DQ8	Hmg-CoA Reductase; Chain: A, B, C, D; Fragment: Catalytic Portion; Ec: 1.1.1.34	432	1.0e-120	MG	
			AAH33692.1	Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase	432	1.0e-120	MG	
NM_008299 NP_032325.1	Mm.3075	U:(C-HI) 2.02	NP_005485.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2	283	3.0e-69	MG	
			XP_052862.4	similar to DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2	257	2.0e-67	MG	
			NP_490647.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a; Heat shock protein J2	252	7.0e-66	MG	
			XP_093388.1	similar to DnaJ homolog subfamily B member 8 (mDJ8)	197	2.0e-49	MG	
NM_010877 NP_035007.1	Mm.10729	U:(C-HI) 2.02	AAM89263.1	p67phox-like protein	826	0	MG	

			P19878	Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH oxidase factor 2) (67 kDa neutrophil oxidase factor) (p67-phox)	825	0	MG	
			NP_000424.1	neutrophil cytosolic factor 2; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); p67phox	824	0	MG	
			AAH01606.1	Similar to neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)	823	0	MG	
			pdb 1HH8	Neutrophil Cytosol Factor 2; Chain: A; Fragment: N-Terminal Domain Residues 1 - 213	346	5.0e-94	MG	
			pdb 1E96	Neutrophil Cytosol Factor 2 (Ncf-2) Tpr Domain, Residues 1-203	332	1.0e-89	MG	
NM_019643	Mm.18637	U:(C-HI) 2.02	NP_067061.1	TERA protein		1.0e-402	110	MG
NP_062617.1								
NM_013594	Mm.22522	U:(C-HI) 2.01, U:(C-D) 2.15	AAD50371.1	methyl-CpG binding protein 1				
NP_038622.1					779	0	MG	
			NP_056671.2	methyl-CpG binding domain protein 1 isoform 1	779	0	MG	
			AAD51442.1	methyl-CpG binding protein splice variant 1	773	0	MG	
			NP_056670.2	methyl-CpG binding domain protein 1 isoform 2	662	0	MG	
			AAD51443.1	methyl-CpG binding protein splice variant 2	657	0	MG	
			NP_056723.2	methyl-CpG binding domain protein 1 isoform PCM1	632	1.0e-179	MG	
			CAA71735.1	methyl-CpG binding protein	625	1.0e-177	MG	
			AAH33242.1	methyl-CpG binding domain protein 1	597	1.0e-169	MG	
			NP_056669.1	methyl-CpG binding domain protein 1 isoform 3	598	1.0e-169	MG	
			NP_002375.1	methyl-CpG binding domain protein 1 isoform 4	526	1.0e-148	MG	
			AAH12487.1	Unknown (protein for MGC:21089)	263	1.0e-68	MG	
NM_025566	Mm.2312	U:(C-HI) 2	NP_689575.1	hypothetical protein MGC17791		1.0e-271	71	MG
NP_079842.1								
			XP_059012.1	similar to RIKEN cDNA 2600017J23	271	1.0e-71	MG	
AK004002	Mm.19844	U:(C-HI) 2	CAA36441.1	five-lipoxygenase activating protein (FLAP)		3.0e-282	75	MG
BAB23117.1								
			NP_001620.2	arachidonate 5-lipoxygenase-activating protein; five-lipoxygenase activating protein; MK-886-binding protein	282	3.0e-75	MG	
			1603359A	lipoxygenase activating protein	279	3.0e-74	MG	
NM_021366	Mm.41170	U:(C-HI) 2	XP_096904.4	similar to Krueppel-like factor 13 (Transcription factor BTEB3) (Basic transcription element binding protein 3) (BTE-binding protein 3) (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Transcription factor NSLP1) (Novel Sp1-like zinc fi		3.0e-306	82	MG
NP_067341.1								



			NP_057079 .1	Kruppel-like factor 13; transcription factor NSLP1; novel Sp1 like zinc finger transcription factor; RANTES factor of late activated T lymphocytes-1; basic transcription element binding protein 3	305	8.0e- 82	MG	
NM_01072 1 NP_034851. 1	Mm.4846	U:(C-D) 7.08	NP_005564 .1	lamin B1	878	0	MG	
			AAH12295. 1	Similar to lamin B1	878	0	MG	
			Q03252	Lamin B2	530	1.0e- 149	MG	
			NP_005563 .1	lamin A/C isoform 2; 70 kDa lamin	522	1.0e- 146	MG	
			P02545	Lamin A/C (70 kDa lamin)	522	1.0e- 146	MG	
			CAA27173. 1	put. lamin A precursor (aa 1-702)	522	1.0e- 146	MG	
			AAH33088. 1	Similar to lamin A/C	414	1.0e- 114	MG	
			A45023	lamin B2 - human (fragment)	403	1.0e- 111	MG	
			AAA36160. 1	lamin A protein	385	1.0e- 105	MG	
NM_02622 8 NP_080504. 1	Mm.30239	U:(C-D) 4.88	NP_071437 .1	up-regulated by BCG-CWS	788	0	MG	
			BAB55268. 1	unnamed protein product	718	0	MG	
			BAA06685. 1	KIAA0082	413	1.0e- 114	MG	
			XP_046677 .3	similar to KIAA0082	413	1.0e- 114	MG	
			AAH15770. 1	Unknown (protein for MGC:23235)	374	1.0e- 102	MG	
			BAA96442. 1	up-regulated by BCG-CWS	244	4.0e- 63	MG	
NM_02615 6 NP_080432. 1	Mm.23739	U:(C-D) 3.75	XP_048364 .2	similar to PP3898	1604	0	MG	
			BAB15807. 1	XAB2	1603	0	MG	
			BAA86491. 1	KIAA1177 protein	1400	0	MG	
			NP_064581 .1	HCNP protein; XPA-binding protein 2	1318	0	MG	
			AAH08778. 1	Similar to HCNP protein; XPA-binding protein 2	1147	0	MG	
			BAB84861. 1	FLJ00081 protein	607	1.0e- 172	MG	
U70139 AAB62717. 1	Mm.86541	U:(C-D) 3.08, U:(HI-D) 2.08	NP_036250 .1	CCR4 carbon catabolite repression 4-like (S. cerevisiae); CCR4-like (carbon catabolite repression 4, S. cerevisiae)	603	1.0e -170	MG	
			AAG01389. 1	nocturnin	554	1.0e -155	MG	
			AAM81188 .1	pol protein	375	1.0e -150	MG	
			AAK11553. 1	polymerase	330	1.0e -132	MG	

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			AAD51797. 1	Gag-Pro-Pol protein	330	1.0e -132	MG	
			AAD21097. 1	polymerase	330	1.0e -132	MG	
			AAA88033. 1	pol/env ORF (bases 3878-8257) first start codon at 4172; Xoc; putative	327	1.0e -131	MG	
			AAK11554. 1	polymerase	327	1.0e -131	MG	
			P10266	Endogenous retrovirus HERV-K10 putative pol polyprotein [Includes: Reverse transcriptase ; Endonuclease]	327	1.0e -131	MG	
			AAD51793. 1	Gag-Pro-Pol-Env protein	327	1.0e -130	MG	
			AAD51796. 1	Gag-Pro-Pol protein	312	1.0e -126	MG	
			AAL60056. 1	pol protein	312	1.0e -126	MG	
			AAG01388. 1	nocturnin	414	1.0e -113	MG	
			AAG18012. 1	gag-pro-pol precursor protein	252	1.0e -113	MG	
			AAC63294. 1	polymerase	167	3.1e -69	MG	
			AAC63291. 1	polymerase	166	8.1e -68	MG	
			AAC63292. 1	polymerase	166	1.1e -67	MG	
			AAC63293. 1	polymerase	163	2.1e -67	MG	
			AAC63290. 1	polymerase	164	3.1e -67	MG	
NM_00813 7 NP_032163. 1	Mm.22322	U;(C-D) 3.01	NP_004288 .1	guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14	686	0	MG	
			AAC50363. 1	GTP-binding protein alpha q subunit	595	1.0e -169	MG	
			AAB64301. 1	GTP-binding protein alpha q	593	1.0e -168	MG	
			P29992	Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)	591	1.0e -168	MG	
			P50148	Guanine nucleotide-binding protein G(q), alpha subunit	589	1.0e -167	MG	
			S71963	GTP-binding protein alpha-q - human (fragment)	589	1.0e -167	MG	
			NP_002058 .1	guanine nucleotide binding protein (G protein), alpha 11 (Gq class); Guanine nucleotide-binding protein, Gq class, GNA11	589	1.0e -167	MG	
			AAB64303. 1	guanine nucleotide binding protein alpha 11 subunit	588	1.0e -167	MG	
			NP_002063 .1	guanine nucleotide binding protein (G protein), q polypeptide; Guanine nucleotide-binding protein (G protein), q; similar to guanine nucleotide binding protein (G protein), q polypeptide (H. sapiens)	588	1.0e -167	MG	
			NP_002059 .i	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	391	1.0e -107	MG	
			XP_009220 .2	similar to GNA15; ALPHA-16	387	1.0e -106	MG	
			XP_095102 .1	similar to Guanine nucleotide-binding protein, alpha-11 subunit (GL2)	369	1.0e -101	MG	

			P29777	Guanine nucleotide-binding protein G(O), alpha subunit 2	353	3.0e-96	MG	
			AAM12609.1	guanine nucleotide binding protein alpha oB	352	6.0e-96	MG	
			P04898	Guanine nucleotide-binding protein G(I), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein)	346	6.0e-94	MG	
			CAB43212.2	hypothetical protein	345	7.0e-94	MG	
5			AAA52556.1	guanine nucleotide-binding regulatory protein alpha-inhibitory subunit	345	7.0e-94	MG	
			NP_002061.1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2; Guanine nucleotide-binding protein (G protein), alpha-	345	7.0e-94	MG	
			NP_066268.1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	342	8.0e-93	MG	
			AAH14627.1	Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	342	8.0e-93	MG	
			AAA52581.1	guanine nucleotide-binding protein alpha-i subunit	341	1.0e-92	MG	
10			NP_002060.3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	341	2.0e-92	MG	
			NP_006487.1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3; 87U6	340	3.0e-92	MG	
			AAA52584.1	guanine nucleotide-binding protein	338	1.0e-91	MG	
			XP_170405.1	similar to Guanine nucleotide-binding protein G(T), alpha-3 subunit (Gustducin alpha-3 chain)	329	7.0e-89	MG	
15	C76314 NP_690023.1	Mm.28270 U:(C-D) 2.97	BAA24862.2	KIAA0432		2.0e-99	MG	
			NP_001244.1	CDC5-like; CDC5 (cell division cycle 5, S. pombe, homolog)-like; Cell division cycle 5, S. pombe, homolog-like; Cdc5-related protein	236	2.0e-99	MG	
			CAC08557.1	dJ319D22.1 (CDC5-like protein)	236	6.0e-95	MG	
20	AK009292 BAB26196.1	Mm.30487 U:(C-D) 2.94, U:(HI-D) 2.87	NP_005085.1	solute carrier family 27 (fatty acid transporter), member 4; fatty acid transport protein 4	561	1.0e-158	MG	
			AAH04268.1	Unknown (protein for IMAGE:3613739)	492	1.0e-138	MG	
			AAH09959.1	Unknown (protein for MGC:16752)	299	7.0e-80	MG	
			BAB55156.1	unnamed protein product	295	1.0e-78	MG	
25			NP_077306.1	solute carrier family 27 member 3; fatty acid transport protein 3	295	1.0e-78	MG	
			NP_054750.1	very long-chain acyl-CoA synthetase homolog 1	286	6.0e-76	MG	
			NP_036386.1	solute carrier family 27 (fatty acid transporter), member 5; very long-chain acyl-CoA synthetase homolog 2; very long-chain acyl-CoA synthetase-related protein; likely ortholog of mouse solute carrier family 27 (fatty acid transporter), member 5	276	6.0e-73	MG	
			NP_003636.1	solute carrier family 27 (fatty acid transporter), member 2; very long-chain fatty-acid-coenzyme A ligase 1; very-long-chain acyl-CoA synthetase	274	3.0e-72	MG	
			AAH03654.1	Similar to hypothetical protein MGC4365	249	8.0e-65	MG	

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M12573 AAA37863. 1	Mm.6388	U:(C-D) 2.94	NP_005336 .2	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1	347	2.0e- 94	MG	
			P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	347	2.0e- 94	MG	
			NP_005337 .1	heat shock 70kDa protein 1B; heat shock 70kD protein 1B	345	6.0e- 94	MG	
			A29160	dnaK-type molecular chaperone HSPA1L	341	2.0e- 92	MG	
			XP_175177 .1	heat shock 70kD protein 1-like	312	6.0e- 84	MG	
			NP_005518 .1	heat shock 70kDa protein 1-like; Heat-shock 70kD protein-like-1	311	1.0e- 83	MG	
			BAA32521. 1	Heat shock protein 70 testis variant	310	3.0e- 83	MG	
			XP_166348 .1	similar to heat shock protein	310	3.0e- 83	MG	
			AAH34483. 1	heat shock 70kD protein 1-like	308	1.0e- 82	MG	
			AAH07276. 1	Similar to heat shock cognate 71-kd protein	301	1.0e- 80	MG	
			AAH15699. 1	Unknown (protein for IMAGE:3906958)	301	1.0e- 80	MG	
			NP_006588 .1	Heat shock protein 70 testis variant	301	1.0e- 80	MG	
			AAH08907. 1	Similar to heat shock 70kD protein 8	301	1.0e- 80	MG	
			NP_068814 .2	heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2	300	1.0e- 80	MG	
			AAH36107. 1	Unknown (protein for MGC:33922)	300	1.0e- 80	MG	
			AAD11466. 1	heat shock protein	300	1.0e- 80	MG	
			CAA36062. 1	heat shock protein 70B' (AA 355-643)	285	1.0e- 75	MG	
			XP_084070 .5	similar to HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B)	285	1.0e- 75	MG	
			AAH35665. 1	heat shock 70kDa protein 6 (HSP70B')	285	1.0e- 75	MG	
			NP_002146 .1	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B'); Heat-shock 70kD protein-6 (HSP70B')	285	1.0e- 75	MG	
AK017185 BAB30625. 1	Mm.26935	U:(C-D) 2.9	Q15771	Ras-related protein Rab-30	401	1.0e- 110	MG	
AK018132 BAB31086. 1	Mm.41370	U:(C-D) 2.44	AAH12375. 1	Similar to KIAA1001 protein	903	0	MG	
			NP_055775 .1	KIAA1001 protein	901	0	MG	
			AAB03341. 1	arylsulfatase A	266	8.0e- 70	MG	
			NP_000478 .2	arylsulfatase A precursor	266	8.0e- 70	MG	
			AAH14210. 1	Similar to arylsulfatase A	266	1.0e- 89	MG	
			pdbj1E2S	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8;	262	2.0e- 68	MG	
			pdbj1E3C	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8;	261	3.0e- 68	MG	

			pdb 1E1Z	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8	261	3.0e-68	MG	
			pdb 1AUK	Human Arylsulfatase A	261	4.0e-68	MG	
			pdb 1E33	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8	257	5.0e-67	MG	
			NP_000503.1	N-acetylgalactosamine-6-sulfatase precursor; Galactosamine (N-acetyl)-6-sulfate sulfatase; chondroitinase	251	3.0e-65	MG	
5			AAH22389.1	Unknown (protein for MGC:24090)	237	5.0e-61	MG	
			NP_004033.1	arylsulfatase F	237	7.0e-61	MG	
			XP_035467.1	similar to arylsulfatase F	235	2.0e-60	MG	
			AAH20229.1	Unknown (protein for MGC:31932)	233	1.0e-59	MG	
			NP_001660.1	arylsulfatase D precursor, isoform a	230	7.0e-59	MG	
10	AK004984 BAB23719.1	Mm.158751 U:(C-D) 2.38	AAA53500.1	cytochrome P450 IID6	186	1.0e-45	MG	
			NP_000097.1	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	186	1.0e-45	MG	
			AAA35737.1	debrisoquine 4-hydroxylase	184	3.0e-45	MG	
15			AAA36403.1	cytochrome P450db1	184	3.0e-45	MG	
	NM_011128 NP_035258.1	Mm.1230 U:(C-D) 2.35, U:(HI-D) 2.73	NP_005387.1	pancreatic lipase-related protein 2	748	0	MG	
20			NP_000927.1	pancreatic lipase	668	0	MG	
			pdb 1LPB	Lipase (E.C. 3.1.1.3) Complexed With Colipase and Inhibited By Undecane Phosphonate Methyl Ester	652	0	MG	
			1604419A	lipase	646	0	MG	
			NP_006220.1	pancreatic lipase-related protein 1	631	1.0e-180	MG	
			AAH25784.1	pancreatic lipase-related protein 1	630	1.0e-179	MG	
25			CAA22264.1	dA149D17.1 (PLRP2 (PNLIPRP2, Pancreatic Lipase Related Protein 2 Precursor, EC 3.1.1.3) LIKE protein)	217	3.0e-55	MG	
	NM_008239 NP_032265.2	Mm.44235 U:(C-D) 2.23, U:(HI-D) 2.15	NP_150285.1	winged helix/forkhead transcription factor	344		MG	
30			AAK00639.1	HNF-3/forkhead-like protein 1	342		MG	
	AK013002 BAB28588.1	U:(C-D) 2.21	AAH00120.1	general transcription factor IIF, polypeptide 1 (74kD subunit)	387	1.0e-106	MG	
			NP_002087.1	general transcription factor IIF, polypeptide 1 (74kD subunit)	387	1.0e-106	MG	
35			CAA45404.1	RAP74	386	1.0e-106	MG	

			pdb 1F3U	Transcription Initiation Factor IIf, Subunit; Chain: A, C, E, G; Fragment: Residues 2-119; Synonym: Transcription Initiation Factor Rap30	315	7.0e-85	MG	
AK007293 BAB24937. 1	Mm.159753	U:(C-D) 2.19, U:(HI-D) 2.62	BAB67772. 1	KIAA1879 protein	189	8.0e-47	MG	
NM_01952 1 NP_062394. 1	Mm.3982	U:(C-D) 2.14	NP_000811 .1	growth arrest-specific 6; AXL stimulatory factor	1075	0	MG	
			NP_000304 .1	protein S (alpha); Protein S, alpha	550	1.0e-155	MG	
			P07225	Vitamin K-dependent protein S precursor	549	1.0e-155	MG	
			AAA60180. 1	protein S alpha	548	1.0e-154	MG	
			AAA60181. 1	protein S precursor	542	1.0e-152	MG	
			CAA31383. 1	pre-protein S (AA -15 to 635)-ttg start	541	1.0e-152	MG	
NM_01169 3 NP_035823. 1	Mm.1021	U:(C-D) 2.08	NP_001069 .1	vascular cell adhesion molecule 1, isoform a precursor; CD106 antigen	1132	0	MG	
			NP_542413 .1	vascular cell adhesion molecule 1, isoform b precursor; CD106 antigen	573	1.0e-162	MG	
			pdb 1VCA	Human Vascular Cell Adhesion Molecule-1; Chain: A, B; Synonym: Vcam-D1,2	303	7.0e-81	MG	
			pdb 1IJ9	Vascular Cell Adhesion Protein 1; Chain: A; Fragment: Vcam-D1, D2 (Integrin Binding Fragment); Synonym: Vcam-1	293	1.0e-77	MG	
			pdb 1VSC	Vascular Cell Adhesion Molecule-1; Chain: A, B; Fragment: N-Terminal Two-Domain Fragment; Synonym: Vcam-1; Engineered: Yes; Mutation: Y196D; Other_Details: Hybrid Molecule Composed Of Vcam-1 Domains 1 and 2 Fused To IgG, Hinge and Fc	290	8.0e-77	MG	
U70210 AAC53593. 1	Mm.5159	U:(C-D) 2.06	XP_051782 .5	similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	1508	0	HG	
			Q92870	Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	1382	0	HG	
			AAH27946. 1	Similar to amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like protein)	629	1.0e-178	HG	
			NP_663722 .1	amyloid beta A4 precursor protein-binding, family B, member 1 isoform delta E9; amyloid beta A4 precursor protein-binding, family B, member 1; stat-like protein; adaptor protein FE65a2	584	1.0e-165	HG	
			NP_001155 .1	amyloid beta A4 precursor protein-binding, family B, member 1 isoform E9; amyloid beta A4 precursor protein-binding, family B, member 1; stat-like protein; adaptor protein FE65a2	579	1.0e-163	HG	
			AAL79526. 1	adaptor protein FE65a2	544	1.0e-153	HG	
			NP_573420 .1	FE65-like protein 2 isoform a; amyloid precursor interacting protein	380	1.0e-104	HG	
			AAH13158. 1	Similar to FE65-LIKE 2	377	1.0e-103	HG	
			NP_573419 .1	FE65-like protein 2 isoform b; amyloid precursor interacting protein	375	1.0e-102	HG	

			NP_573418 .1	FE65-like protein 2 isoform c; amyloid precursor interacting protein	374	1.0e-102	HG	
			NP_006042 .2	FE65-like protein 2, isoform a; amyloid precursor interacting protein	373	1.0e-101	HG	
NM_02027 7 NP_064673. 1	Mm.143747	U:(C-D) 2.05, U:(H1-D) 2.32	NP_055370 .1	transient receptor potential cation channel, subfamily M, member 5; MLN1 and TRP-related; MLN1- and TRP-related	1875	0		MG
			CAB66342. 1	LTRPC5 protein	1875	0		MG
			NP_060106 .2	transient receptor potential cation channel, subfamily M, member 4	833	0		MG
			AAL02142. 1	TRP-related cation influx channel	728	0		MG
			BAA90907. 1	unnamed protein product	726	0		MG
			BAA95563. 1	transient receptor potential-related channel 7, a novel putative Ca2+ channel protein	696	0		MG
			NP_003298 .1	transient receptor potential cation channel, subfamily M, member 2; transient receptor potential-related channel 7, a novel putative Ca2+ channel protein; transient receptor potential channel 7	696	0		MG
			CAD01139. 1	putative TRP cation channel	688	0		MG
			BAB86335. 1	LTRPC8	510	1.0e-143		MG
			NP_076985 .3	transient receptor potential cation channel, subfamily M, member 8	510	1.0e-143		MG
			NP_060132 .3	transient receptor potential cation channel, subfamily M, member 6	398	1.0e-109		MG
			AAK19738. 2	channel-kinase 1	317	7.0e-85		MG
			XP_030709 .6	similar to LTRPC7	317	7.0e-85		MG
			BAB15429. 1	unnamed protein product	295	3.0e-78		MG
			AAC80000. 1	melastatin 1	270	1.0e-70		MG
			NP_002411 .2	transient receptor potential cation channel, subfamily M, member 1; melastatin 1 [	270	1.0e-70		MG
NM_01992 2 NP_064306. 1	Mm.20904	U:(C-D) 2.05	AAH08745. 1	cartilage associated protein	666	0		MG
			NP_006362 .1	cartilage associated protein; cartilage-associated protein	666	0		MG
			BAC03743. 1	unnamed protein product	633	1.0e-180		MG
			CAC16786. 1	nucleolar protein No55	403	1.0e-111		MG
			NP_006446 .1	nucleolar autoantigen (55kD) similar to rat synaptonemal complex	402	1.0e-111		MG
NM_01167 6 NP_035806. 1	Mm.27744	U:(C-D) 2.04	NP_005139 .1	unc119 (C.elegans) homolog, isoform a; unc119 (C.elegans) homolog; retinal protein 4	391	1.0e-108		MG
			NP_473376 .1	unc119 (C.elegans) homolog, isoform b; unc119 (C.elegans) homolog; retinal protein 4	317	2.0e-85		MG

5	AF241249 AAG02285. 1	Mm.35241	U:(C-D) 2.03	AAH23549. 1	Unknown (protein for MGC:18590)	788	0	MG	
				AAH07570. 1	Unknown (protein for IMAGE:3029289)	828	1.0e-178	MG	
				BAB84871. 1	FLJ00103 protein	516	1.0e-144	MG	
				XP_036104. 4	similar to FLJ00103 protein	504	1.0e-141	MG	
				AAH12332. 1	Unknown (protein for MGC:20519)	430	1.0e-118	MG	
				BAB47492. 1	KIAA1863 protein	396	1.0e-109	MG	
				BAB71400. 1	unnamed protein product	303	2.0e-80	MG	
10	NM_01022 0	Mm.154390	U:(C-D) 2.02	NP_004108 .1	FK506-binding protein 5; 51 kDa FK506-binding protein 5; 54 kDa progesterone receptor-associated immunophilin; T-cell FK506-binding protein; peptidylprolyl cis-trans isomerase; rotamase; FF1 antigen; HSP90-binding immunophilin	783	0	MG	
	NP_034350. 1			AAA86245. 1	FKBP54	770	0	MG	
				NP_002005 .1	FK506-binding protein 4; FK506-binding protein 4 (59kD); T-cell FK506-binding protein, 59kD; p59 protein; HSP binding immunophilin; peptidylprolyl cis-trans isomerase; rotamase; FK506 binding protein 4 (59kD)	498	1.0e-139	MG	
				XP_095921 .1	similar to FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)	343	7.0e-93	MG	
				XP_172777 .1	similar to FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase FKBP4) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)	323	6.0e-87	MG	
				AAH02887. 1	Similar to FK506-binding protein 4 (59kD)	323	1.0e-86	MG	
20	NM_01669 6	Mm.24193	U:(C-D) 2.02	NP_002072 .1	glypican 1 precursor	934	0	MG	
	NP_057905. 1			NP_005699 .1	glypican 6 precursor	490	1.0e-137	MG	
				NP_001439 .2	glypican 4	445	1.0e-123	MG	
				O75487	Glypican-4 precursor (K-glypican)	444	1.0e-123	MG	
				AAC69991. 1	glypican-4	443	1.0e-123	MG	
				CAB39178. 1	GPC4 (glypican 4)	409	1.0e-112	MG	
				XP_168232 .2	similar to Glypican-2 precursor (Cerebroglycan) (HSPG M13)	362	3.0e-98	MG	
25									
30	NM_01369 2	Mm.4292	U:(C-D) 2.01	NP_005646 .1	TGFB inducible early growth response	742	0	MG	
	NP_038720. 1			A57531	EGR alpha transcription factor - human	723	0	MG	



			NP_003588 .1	TGFB inducible early growth response 2	265	3.0e-69	MG	
AK004865 BAB23626. 1	Mm.10633	U:(C-D) 2	NP_005509 .1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	929	0	MG	
			AAA92674. 1	HMG CoA synthase	679	0	MG	
			NP_002121 .1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	659	0	MG	
			S27197	hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform	650	0	MG	
			BAC04559. 1	unnamed protein product	629	1.0e-179	MG	
			XP_060842 .1	similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)	244	4.0e-63	MG	
			AAA92673. 1	HMG CoA synthase	240	1.0e-61	MG	
NM_01981 0 NP_062784. 1	Mm.25237	U:(C-D) 2	NP_000334 .1	solute carrier family 5 (sodium/glucose cotransporter), member 1; Human Na <sup>+</sup> /glucose cotransporter 1 mRNA, complete cds; solute carrier family 5 (sodium/glucose transporter), member 1	1024	0	MG	
			NP_055042 .1	solute carrier family 5 (low affinity glucose cotransporter), member 4; solute carrier family 5 (neutral amino acid transporters, system A), member 4; low affinity sodium glucose cotransporter	856	0	MG	
			I909123A	Na glucose cotransporter	709	0	MG	
			NP_003032 .1	solute carrier family 5 (sodium/glucose cotransporter), member 2; solute carrier family 5 (sodium/glucose transporter), member 2	709	0	MG	
			AAL66409. 1	sodium/glucose cotransporter	700	0	MG	
			CAC00574. 1	dJ1024N4.1 (novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1))	583	1.0e-165	MG	
			NP_443176 .2	sodium/myo-inositol cotransporter 2; putative sodium-coupled cotransporter RKST1; homolog of rabbit KST1	575	1.0e-162	MG	
			AAK97053. 1	putative sodium-coupled cotransporter RKST1	574	1.0e-162	MG	
			XP_064487 .3	ilar to 597 aa protein related to Na/glucose cotransporters	540	1.0e-152	MG	
			CAB06090. 2	fF65B7.1 (solute carrier family 5 (sodium/glucose cotransporter), member 1 (SGLT1, High Affinity Sodium-Glucose Cotransporter))	512	1.0e-143	MG	
			P53794	Sodium/myo-inositol cotransporter (Na <sup>+</sup> /myo-inositol cotransporter)	511	1.0e-143	MG	
			NP_008864 .1	solute carrier family 5 (inositol transporters), member 3; solute carrier family 5 (inositol transporter), member 3; human solute carrier family 5, member 3, Sodium/myo-inositol cotransporter; sodium/myo-inositol cotransporter 1	510	1.0e-143	MG	
			NP_689564 .1	hypothetical protein FLJ25217	399	1.0e-110	MG	
NM_02878 0 NP_083056. 1	Mm.29649	U:(C-D) 2	NP_006396 .2	transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1	1091	0	MG	
			O15321	Transmembrane 9 superfamily protein member 1 precursor (hMP70)	1081	0	MG	

			AAF21983.1	SM-11044 binding protein	313	1.0e-83	MG	
			XP_050993.1	similar to Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)	313	1.0e-83	MG	
			AAF98159.1	transmembrane protein TM9SF3	312	1.0e-83	MG	
			BAB55369.1	unnamed protein product	305	2.0e-81	MG	
5			NP_055557.1	KIAA0255 gene product	291	2.0e-77	MG	
			NP_064508.1	endomembrane protein emp70 precursor isolog	285	2.0e-69	MG	
			NP_004791.1	transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2	265	2.0e-69	MG	
			BAA91362.1	unnamed protein product	248	4.0e-64	MG	
			BAC11232.1	unnamed protein product	227	7.0e-58	MG	
10	NM_009252	Mm.22650	U:(C-D) 1.77	CAA48671.1	alpha1-antichymotrypsin	497	1.1e-138	MG
				XP_028322.1	similar to Alpha-1-antichymotrypsin precursor (ACT)	494	1.0e-138	MG
15				AAH34554.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	493	1.0e-138	MG
				ITHUC	alpha-1-antichymotrypsin precursor - human	482	1.0e-135	MG
				AAD08810.1	alpha-1-antichymotrypsin precursor	481	1.0e-134	MG
				AAA51560.1	alpha-1-antichymotrypsin precursor	471	1.0e-131	MG
				pdb 1QMN	alpha - 1-Antichymotrypsin	461	1.0e-128	MG
20				I313184C	chymotrypsin inhibitor	439	1.0e-122	MG
				pdb 2ACH	alpha1 Antichymotrypsin	438	1.0e-121	MG
				NP_001076.1	alpha-1-antichymotrypsin, precursor; alpha-1-antichymotrypsin; antichymotrypsin	437	1.0e-121	MG
				pdb 3CAA	Cleaved Antichymotrypsin A347R	426	1.0e-118	MG
				pdb 1AS4	Cleaved Antichymotrypsin A349R	426	1.0e-118	MG
25				pdb 4CAA	Cleaved Antichymotrypsin T345R	426	1.0e-118	MG
				NP_006206.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4; protease inhibitor 4 (kallistatin)	310	6.0e-83	MG
				P29622	Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4)	310	6.0e-83	MG
				NP_000615.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)	307	3.0e-82	MG
				T12502	hypothetical protein DKFZp434P131.1	307	3.0e-82	MG

			AAB60386.1	protein C inhibitor	307	4.0e-82	MG	
			AAA35688.1	plasma serine protease inhibitor precursor	307	4.0e-82	MG	
			pdb1ATU	Uncleaved alpha-1-Antitrypsin	305	2.0e-81	MG	
			pdb1KCT	Alpha 1-Antitrypsin	305	2.0e-81	MG	
5			NP_000286.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	305	2.0e-81		MG
			I313184B	alpha1 antitrypsin	304	3.0e-81	MG	
			AAA51547.1	alpha-1-antitrypsin precursor	304	3.0e-81	MG	
			AAH15642.1	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	304	3.0e-81		MG
			AAA51546.1	alpha-1-antitrypsin	303	5.0e-81	MG	
10			AAB26244.2	acrosomal serine protease inhibitor	303	6.0e-81	MG	
			P01009	Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (PRO0684/PRO2209)	303	6.0e-81		MG
	NM_013850 NP_038878.1	Mm.103351 U:(C-IR)+2.4	AAK00959.1					
15				ABC transporter member 7	3108	0		
			AAN04657.1	ABC transporter ABCA7	3108	0		
			NP_061985.1	ATP-binding cassette, sub-family A, member 7, isoform a; autoantigen SS-N; macrophage ABC transporter	3105	0		
			NP_150651.1	ATP-binding cassette, sub-family A, member 7, isoform b; autoantigen SS-N; macrophage ABC transporter	2904	0		
			AAF98175.1	ATP-binding cassette transporter 1	1923	0		
			NP_005493.2	ATP-binding cassette, sub-family A member 1; ATP-binding cassette 1; high density lipoprotein deficiency, Tangier type, 1; cholesterol efflux regulatory protein	1922	0		
20			AAK43526.1	ATP-binding cassette 1 sub-family A member 1	1921	0		
			AAF86276.1	ABCA1	1918	0		
			O95477	ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux regulatory protein).	1916	0		
			CAA10005.1	ATP-binding cassette transporter-1 (ABC-1)	1916	0		
			P78363	Retinal-specific ATP-binding cassette transporter (RIM ABC transporter) (RIM protein) (RMP) (Stargardt disease protein).	1845	0		
25			AAC05632.1	rim ABC transporter	1844	0		
			CAA75729.1	ABCR	1840	0		

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			AAC23915. 1	ATP-binding cassette transporter	1636	0
			NP_000341 .1	ATP-binding cassette, sub-family A member 4; ATP binding cassette transporter; ATP-binding transporter, retina-specific; rim protein	1630	0
			NP_775099 .1	ATP-binding cassette, sub-family A, member 12 isoform a; ATP-binding cassette A12	972	0
			NP_056472 .2	ATP-binding cassette, sub-family A, member 12 isoform b; ATP-binding cassette A12	972	0
			AAN40735. 1	ATP-binding cassette transporter family A member 12	971	0
			AAK54355. 1	ATP-binding cassette transporter family A member 12	968	0
			AAO59914. 1	ATP binding cassette transporter A13	924	0
			AAD49852. 1	ATP cassette binding transporter 1	794	0
			XP_00129 0.5	ATP-binding cassette, sub-family A member 4	731	0
			A59189	ATP-binding cassette transporter	635	0
			AAH08755. 1	Similar to KIAA1062 protein	635	0
			BAA83014. 2	KIAA1062 protein	635	0
			NP_001597 .1	ATP-binding cassette, sub-family A, member 2	635	0
			Q9BZC7	ATP-binding cassette, sub-family A, member 2 (ATP-binding cassette transporter 2) (ATP-binding cassette 2).	632	1.00e -180
			T46467	hypothetical protein DKFZp434E1030....	461	1.00e -129
			NP_001080 .1	ATP-binding cassette, sub-famil...	440	1.00e -122
			S71363	probable ATP-binding cassette transp...	440	1.00e -122
			AAD49851. 1	ATP cassette binding transporter ...	390	1.00e -107
			T47150	hypothetical protein DKFZp547P193.1	353	2.00e -98
			AAF06727. 1	autoantigen SS-N	239	5.00e -62
			CAD54757. 1	ABCA5 transporter	233	2.00e -60
			CAB93535 .3	ATP-binding cassette protein	233	3.00e -60
			AAK30022. 1	ATP-binding cassette A5	233	3.00e -60
			NP_061142 .2	ATP-binding cassette, sub-family A, member 5; ATP-binding cassette A5	233	3.00e -60
			NP_689914 .1	hypothetical protein FLJ33951	229	4.00e -59
			NP_525022 .2	ATP-binding cassette, sub-family A, member 9 isoform a; ATP-binding cassette A9	229	4.00e -59
			AAK30024. 1	ATP-binding cassette A9	229	5.00e -59
			AAK30025. 1	ATP-binding cassette A10	226	4.00e -58
			NP_525021 .2	ATP-binding cassette, sub-family A, member 10; ATP-binding cassette A10	224	2.00e -57
			NP_759018 .1	ATP-binding cassette, sub-family A, member 9 isoform b; ATP-binding cassette A9	223	4.00e -57

			NP_525023.2	ATP-binding cassette, sub-family A, member 6 isoform a; ATP-binding cassette A6; ABC transporter ABCA6	222	5.00e-57
			AAM77557.1	ABC transporter ABCA6	222	6.00e-57
			BAC04994.1	unnamed protein product	220	2.00e-56
			AAK30023.1	ATP-binding cassette A6	220	2.00e-56
5			NP_009099.1	ATP-binding cassette, sub-family A member 8	219	3.00e-56
			BAB71359.1	unnamed protein product	213	3.00e-54
			BAB71208.1	unnamed protein product	209	3.00e-53
			BAB67781.1	KIAA1888 protein	208	7.00e-53
10			BAC11021.1	unnamed protein product	204	1.00e-51

Subtable 1C - Mixed (Favorable and Unfavorable)

	Mouse Gene Protein	Unigene	Behavior	Human Protein	Human Protein Name	Score	E-Value	BLAST x	
5	AK007530 BAB2509 1.1	Mm.46315	F:(C-HI) -7.8, F:(C-D) -2.61, U:(HI-D) 2.99	NP_00395 1.2	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene	190	2.00e-48	MG	
				NP_05743 1.1	putative N-acetyltransferase Camello 2	189	4.00e-48	MG	
				BAA7164 3.1	GLA	189	4.00e-48	MG	
10				AAH1262 6.1	kidney- and liver-specific gene	188	1.00e-47	MG	
				T44342	hypothetical protein TSC501 [imported]	188	1.00e-47	MG	
15	NM_0078 25 NP_03185 1.1	Mm.4781	F:(C-HI) -6.41, U:(HI-D) 5.83	AAC9542 6.1	oxysterol 7alpha-hydroxylase	640	0	MG	
				NP_00481 1.1	cytochrome P450, subfamily VIIB, polypeptide 1; oxysterol 7alpha-hydroxylase	640	0	MG	
				P22680	Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase)	313	5.00e-85	MG	
20	NM_0157 63 NP_05657 8.1	Mm.28548	F:(C-HI) -3.7, U:(C-D) 3.14	Q14693	Lipin 1	149 3	0	MG	
				NP_66373 1.1	lipin 1	148 8	0	MG	
				AAH3053 7.1	Similar to lipin 1	148 7	0	MG	
				XP_04113 6.4	similar to Hypothetical protein KIAA0188	147 6	0	MG	
25				NP_05546 1.1	lipin 2	790	0	MG	
	X71479 CAA5058 5.1		F:(C-HI) -3.57, F:(C-D) -2.54, U:(HI-D) 2.82	CAA5058 6.1	cytochrome P450	268	2.00e-72	MG	
				NP_00076 9.1	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase	267	4.00e-72	MG	
30				I65981	fatty acid omega-hydroxylase (EC 1.14.15.-) cytochrome P450 4A11 - human	267	4.00e-72	MG	

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			Q02928	Cytochrome P450 4A11 precursor (CYP1A11) (Fatty acid omega-hydroxylase) (P-450 HK omega) (Lauric acid omega-hydroxylase) (CYP4A11) (P450-HL-omega)	265	2.00e-71	MG	
			BAA0286 4.1	fatty acid omega-hydroxylase	265	2.00e-71	MG	
			AAF7672 2.1	fatty acid omega-hydroxylase CYP4A11	261	1.00e-70	MG	
			CAB7210 5.1	dJ18D14.4 (cytochrome P450, subfamily IVA, polypeptide 11)	253	6.00e-68	MG	
			BAC0375 1.1	unnamed protein product	202	1.00e-52	MG	
			AAH2810 2.1	Unknown (protein for MGC:40051)	202	1.00e-52	MG	
NM_007643 NP_031669.1	Mm.18628	F:(C-HI) -3.03, U:(C-D) 2.05, U:(HI-D) 3.33	P16671	Platelet glycoprotein IV (GPIV) (GPIIB) (CD36 antigen) (PAS IV) (PAS-4 protein)	798	0	MG	
			NP_00006 3.1	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I)	796	0	MG	
			I59613	cell adhesion receptor CD36	791	0	MG	
			AAM1463 6.1	CD36 antigen (collagen type I receptor, thrombospondin receptor)	780	0	MG	
			NP_00549 7.1	scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor) -; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	271	3.00e-72	MG	
			A56525	lysosomal integral membrane protein II - human	271	3.00e-72	MG	
			NP_00549 6.2	scavenger receptor class B, member 1; CD36 antigen-like 1; scavenger receptor class B type 1; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	255	2.00e-67	MG	
			A48528	membrane glycoprotein CLA-1 protein long form precursor - human	252	2.00e-68	MG	
AK007264 BAB24924.1	Mm.200370	F:(C-HI) -2.95, U:(HI-D) 2.34	AAD1222 7.1	similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)	447	1.00e-125	MG	
			XP_08723 0.2	similar to Uridine phosphorylase (UDRPase)	428	1.00e-120	MG	
			NP_00335 5.1	uridine phosphorylase	316	3.00e-86	MG	
NM_010379 NP_034509.1	Mm.6716	F:(C-HI) -2.87, U:(HI-D) 2.37	I54432	MHC class II histocompatibility antigen DQw1-beta chain precursor	347	1.00e-95	MG	
			I67725	cell surface glycoprotein - human	347	1.00e-95	MG	
			AAA9233 2.1	MHC class II HLA-DQ-beta-1	342	4.00e-94	MG	
			NP_00211 4.1	major histocompatibility complex, class II, DQ beta 1 precursor	340	1.00e-93	MG	
			AAA9233 1.1	MHC class II HLA-DQ-beta-1	340	1.00e-93	MG	

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			P05537	HLA class II histocompatibility antigen, DQ(W3) beta chain precursor	338	5.00e-93	MG	
			AAB4123 1.1	MHC class II HLA-DQ	338	5.00e-93	MG	
			P01920	HLA class II histocompatibility antigen, DQ(3) beta chain precursor (Clone II-102)	337	1.00e-92	MG	
			AAA5976 8.1	HLA-DQB1	337	1.00e-92	MG	
			I55996	MHC HLA-DQ-beta cell surface glycoprotein - human	335	3.00e-92	MG	
			AAC4196 6.1	MHC class II HLA-DQ-beta-1	335	4.00e-92	MG	
			AAF2831 5.1	MHC class II antigen	333	2.00e-91	MG	
			AAC4196 4.1	MHC class II HLA-DQ-beta-1	333	2.00e-91	MG	
			AAC4196 5.1	MHC class II HLA-DQ-beta-1	332	4.00e-91	MG	
			P03992	HLA class II histocompatibility antigen, DQB1*0602 beta chain precursor (DQ(5)) (DC-1)	331	6.00e-91	MG	
			AAA5977 2.1	lymphocyte antigen	329	3.00e-90	MG	
			I68718	MHC class II histocompatibility antigen DQ-beta chain precursor - human	328	4.00e-90	MG	
			B37044	MHC class II histocompatibility antigen HLA-DQ beta chain (DQ4) precursor - human	328	4.00e-90	MG	
			P05538	HLA class II histocompatibility antigen, DX beta chain precursor	328	4.00e-90	MG	
			CAA6528 0.1	human leukocyte antigen-DQ beta chain	328	7.00e-90	MG	
			AAC4197 3.1	MHC class II HLA-DQ-beta-1	328	7.00e-90	MG	
			AAC4197 4.1	MHC class II HLA-DQ-beta-1	327	9.00e-90	MG	
NM_0205 64 NP_06558 9.1	Mm.6562	F:(C-HI) -2.84, F:(C-D) -2.36, U:(HI-D) 2.6	AAC7855 3.1	hydroxysteroid sulfotransferase SULT2B1a	228	1.00e-59	MG	
			NP_00459 6.1	sulfotransferase family, cytosolic, 2B, member 1; sulfotransferase family 2B, member 1	228	1.00e-59	MG	
			AAC7849 9.1	hydroxysteroid sulfotransferase SULT2B1b	228	1.00e-59	MG	
			21465697	Chain A, Crystal Structure Of Human Dehydroepiandrosterone Sulfotransferase In Complex With Substrate	218	1.00e-56	MG	
NM_0324 00 NP_11577 6.1	Mm.12511 0	F:(C-HI) -2.79, U:(HI-D) 3.03	AAL9569 0.1	P2Y purinoceptor 1	474	1.00e-133	MG	
			NP_14903 9.1	G protein-coupled receptor 91	474	1.00e-133	MG	



5	NM_0084 95 NP_03252 1.1	Mm.43831	F:(C-HI) -2.65, U:(C-D) 2.32	NP_00229 6.1	beta-galactosidase binding lectin precursor; Lectin, galactose-binding, soluble, 1; galectin	259	2.00e- 69	MG	
				1713410A	beta galactoside soluble lectin	257	6.00e- 69	MG	
10	AK003129 BAB2258 9.1	Mm.2368	F:(C-HI) -2.51, F:(C-D) -3.41, U:(HI-D) 3.46	AAH0029 4.1	Unknown (protein for IMAGE:2819455)	241	8.00e- 64	MG	
				NP_00632 6.1	translocase of inner mitochondrial membrane 17 homolog A (yeast); preprotein translocase	239	3.00e- 63	MG	
15	NM_0115 96 NP_03572 6.1	Mm.1158	F:(C-HI) -2.51, F:(C-D) -2.34, U:(HI-D) 4.16	NP_03659 5.1	TJ6 protein	147 9	0	MG	
				AAH3239 8.1	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 1	811	0	MG	
				NP_00516 8.2	ATPase, H <sup>+</sup> transporting, lysosomal, non-catalytic accessory protein 1A, 110/116 kDa subunit; ATPase, H <sup>+</sup> transporting, lysosomal non-catalytic accessory protein 1 (110/116kD); vacuolar proton pump, subunit 1; clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit; vacuolar proton translocating ATPase 116 kDa subunit A isoform 1; vacuolar adenosine triphosphatase subunit Ac116; H(+)-transporting two-sector ATPase, 116 kDa accessory protein A1; vacuolar-type H(+)-ATPase 115 kDa subunit	809	0	MG	
				CAA9607 7.1	vacuolar-type H(+)-ATPase 115 kDa subunit	806	0	MG	
				NP_06568 3.1	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 4; vacuolar proton pump 116 kDa accessory subunit; vacuolar proton pump, subunit 2; H(+)-transporting two-sector ATPase, noncatalytic accessory protein 1B; ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B; renal tubular acidosis; ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 2 (38kD)	787	0	MG	
				NP_00601 0.2	T-cell, immune regulator 1, isoform a; ATPase, H <sup>+</sup> transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis	766	0	MG	

			Q13488	Vacuolar proton translocating ATPase 116 kDa subunit A isoform 3 (V-ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit) (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune response cDNA7 protein) (TIRC7)	784	0	MG	
			AAA9787 8.1	specific 116-kDa vacuolar proton pump subunit	757	0	MG	
			AAH2230 0.1	Unknown (protein for MGC:22527)	640	0	MG	
			NP_00604 4.1	T-cell, immune regulator 1, isoform b; ATPase, H <sup>+</sup> transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis	609	1.00e-174	MG	
AF193796 AAL09298 .1	Mm.20706 2	F:(C-HI) -2.33, U:(HI-D) 3.03	XP_00680 4.2	similar to Homeobox protein Hox-C13 (Hox-3G)	505	1.00e-142	MG	
			NP_05910 6.1	homeo box C13	504	1.00e-142	MG	
			BAB1478 6.1	unnamed protein product	280	7.00e-75	MG	
NM_0167 04 NP_05791 3.1	Mm.20247	F:(C-HI) -2.26, U:(HI-D) 3.29	NP_00005 6.1	Complement component 6 precursor	124 9	0	MG	
			A34372	complement C6 precursor [validated]	124 6	0	MG	
			XP_17050 8.1	similar to Complement component C6 precursor	916	0	MG	
			AAB5943 3.1	complement component C6	760	0	MG	
			NP_00057 8.1	complement component 7 precursor	397	1.00e-110	MG	
			CAA6012 1.1	complement C7	394	1.00e-109	MG	
NM_0078 70 NP_03189 6.1	Mm.10287	F:(C-HI) -2.2, U:(HI-D) 2.24	NP_00493 5.1	deoxyribonuclease I-like 3	506	1.00e-143	MG	
			AAC2365 2.1	DNase gamma	504	1.00e-143	MG	
			BAA1184 1.1	deoxyribonuclease I precursor	237	2.00e-62	MG	
			NP_00521 4.2	deoxyribonuclease I	237	3.00e-62	MG	
			NP_00136 5.1	deoxyribonuclease I-like 2	226	5.00e-59	MG	
			NP_00672 1.1	deoxyribonuclease I-like 1	224	1.00e-58	MG	
			AAB0049 6.1	DNL1L gene product	224	1.00e-58	MG	
			AAB0049 5.1	DNase I	221	1.00e-57	MG	

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NM_0101 87 NP_03431 7.1	Mm.10809	F:(C-HI) -2.18, U:(HI-D) 2.55	AAD0063 8.1	Fc-gamma-RIIb2	309	6.00e- 84	MG	
			AAD0064 1.1	Fc-gamma-RIIb2	306	6.00e- 83	MG	
			CAA3671 3.1	precursor polypeptide (AA -42 to 249)	305	8.00e- 83	MG	
			AAA3584 2.1	IgG Fc fragment receptor precursor	304	2.00e- 82	MG	
			AAA3605 1.1	IgG Fc receptor beta-Fc-gamma-RII	301	1.00e- 81	MG	
			CAA3564 4.1	IgG Fc receptor	301	2.00e- 81	MG	
			AAD0063 9.1	Fc-gamma-RIIb1	301	2.00e- 81	MG	
			AAD0063 7.1	Fc-gamma-RIIb1	301	2.00e- 81	MG	
			AAD0064 0.1	Fc-gamma-RIIb1	297	3.00e- 80	MG	
			P31994	Low affinity immunoglobulin gamma FC region receptor II-B precursor (FC-gamma RII-B) (FCRII-B) (IGG FC receptor II-B) (FC-gamma-RIIB) (CD32) (CDW32)	297	3.00e- 80	MG	
			NP_00399 2.2	Fc fragment of IgG, low affinity IIb, receptor for (CD32); Fc fragment of IgG, low affinity II, receptor for (CD32)	296	4.00e- 80	MG	
			JL0119	Fc gamma (IgG) receptor IIb precursor - human	296	1.00e- 80	MG	
NM_0074 72 NP_03149 8.1	Mm.18625	F:(C-HI) -2.17, U:(HI-D) 2.38	I52366	uterine water channel - human	496	1.00e- 140	MG	
			AAH2248 6.1	aquaporin 1 (channel-forming integral protein, 28kD)	495	1.00e- 139	MG	
			NP_00037 6.1	aquaporin 1; aquaporin 1 (channel-forming integral protein, 28kDa); Aquaporin-1 (channel-forming integral protein, 28kDa); Colton blood group	495	1.00e- 139	MG	
			AAI8713 6.1	aquaporin 1	488	1.00e- 137	MG	
			AAC5064 9.1	channel-like integral membrane protein	293	7.00e- 79	MG	
			AAC2378 8.1	aquaporin	276	8.00e- 74	MG	
			AAC0316 8.1	putative alternative lens membrane intrinsic protein	238	2.00e- 62	MG	
			NP_03619 6.1	major intrinsic protein of lens fiber; aquaporin	233	1.00e- 60	MG	
			NP_00047 7.1	aquaporin 2; Aquaporin-2 (collecting duct)	230	9.00e- 60	MG	
			AAB3026 8.1	hAQP-CD=collecting duct aquaporin [human, kidney, Peptide, 271 aa]	228	3.00e- 59	MG	
			I51877	water-channel aquaporin 2 - human	227	7.00e- 59	MG	
			I64818	water-channel aquaporin 2 - human	227	7.00e- 59	MG	
			AAC1648 1.1	aquaporin (water channel protein)	223	1.00e- 57	MG	

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			NP_00401 9.1	aquaporin 4 C2 isoform; mercurial-insensitive water channel	221	3.00e-57	MG	
			NP_00164 1.1	aquaporin 4 isoform a; mercurial-insensitive water channel	221	3.00e-57	MG	
			I39177	mercurial-insensitive water channel - human	221	4.00e-57	MG	
			I39178	aquaporin 4, long splice form - human	221	4.00e-57	MG	
			NP_00164 2.1	aquaporin 5; Aquaporin-5	218	5.00e-56	MG	
NM_0100 24 NP_03415 4.1	Mm.19987	F:(C-HI) -2.14, F:(C-D) -2.01, U:(HI-D) 2.28	NP_00191 3.2	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2); Dopachrome tautomerase (dopachrome delta-isomerase; tyrosinase-related protein 2)	883	0	MG	
			CAA3578 5.1	pre propeptide (AA -24 to 503)	502	1.00e-141	MG	
			NP_00054 1.1	tyrosinase-related protein 1	502	1.00e-141	MG	
			CAD1332 8.1	bA3L8.1 (tyrosinase-related protein 1)	498	1.00e-140	MG	
			NP_00036 3.1	tyrosinase (oculocutaneous albinism IA); Tyrosinase	402	1.00e-112	MG	
AF385682 AAK6236 3.1	Mm.27242	F:(C-HI) -2.04, U:(HI-D) 2.02	NP_07144 2.1	EGF-TM7-latrophilin-related protein	934	0	MG	
			BAA3448 8.1	KIAA0768 protein	359	2.00e-98	MG	
			NP_05605 1.1	lectomedin-3	348	4.00e-95	MG	
			AAD5467 6.1	lectomedin-1 beta	341	4.00e-93	MG	
			NP_03643 4.1	latrophilin 1; KIAA0786 protein; lectomedin-1; latrophilin	341	4.00e-93	MG	
			AAD5467 5.1	lectomedin-1 alpha	341	4.00e-93	MG	
			BAA3450 6.1	KIAA0786 protein	337	8.00e-92	MG	
			AAG2746 1.1	lectomedin-2	330	1.00e-89	MG	
			NP_05573 6.1	lectomedin-2; KIAA0821 protein	330	1.00e-89	MG	
			AAH0758 7.1	Unknown (protein for IMAGE:3162852)	322	2.00e-87	MG	
			NP_69088 0.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform b	281	4.00e-75	MG	
			NP_00177 5.2	CD97 antigen, isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein	280	2.00e-74	MG	
			NP_11596 0.1	egf-like module-containing mucin-like receptor 3 isoform a	278	5.00e-74	MG	
			AAF2197 4.1	EGF-like module EMR2	277	8.00e-74	MG	
			NP_03847 5.2	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform a	275	4.00e-73	MG	
			BAC0614 6.1	seven transmembrane helix receptor	275	4.00e-73	MG	

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			I37225	leucocyte antigen CD97	275	4.00e-73	MG	
			NP_51096 6.1	CD97 antigen, isoform 1 precursor; leukocyte antigen CD97; seven-span transmembrane protein	265	3.00e-70	MG	
			AAB3668 2.1	CD97	265	3.00e-70	MG	
			BAC0617 8.1	seven transmembrane helix receptor	265	3.00e-70	MG	
			BAC0613 3.1	seven transmembrane helix receptor	260	1.00e-68	MG	
			P48960	Leucocyte antigen CD97 precursor	260	1.00e-68	MG	
			NP_00196 5.1	egf-like module containing, mucin-like, hormone receptor-like sequence 1; egf-like module containing, mucin-like, hormone receptor-like	259	2.00e-68	MG	
			NP_69088 1.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform c	254	7.00e-67	MG	
			NP_69088 3.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform e	231	6.00e-60	MG	
			NP_69088 2.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform d	231	6.00e-60	MG	
			NP_69088 5.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform g	231	6.00e-60	MG	
			NP_69088 4.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform f	231	6.00e-60	MG	
			AAC0517 2.1	R29368_2	225	4.00e-58	MG	
	NM_010016 NP_03414 6.1	Mm.20236 F:(C-HI) -2.04, U:(HI-D) 2.14	NP_00056 5.1	decay accelerating factor for complement (CD55, Cromer blood group system); Decay-accelerating factor of complement	367	1.00e-101	MG	
			P08174	Complement decay-accelerating factor precursor (CD55 antigen)	365	1.00e-101	MG	
			AAA5216 7.1	decay-accelerating factor precursor	364	1.00e-100	MG	
			AAB4862 2.1	decay-acceleration factor	363	1.00e-100	MG	
			A26359	decay-accelerating factor, splice form 1 precursor - human	355	1.00e-97	MG	
			23200413	Chain R, Structural Model Of Human Decay-Accelerating Factor Bound To Echovirus 7 From Cryo-Electron Microscopy	308	8.00e-64	MG	
			AAL2583 3.1	decay-accelerating factor 1 ab	243	6.00e-64	MG	
			AAL2583 5.1	decay-accelerating factor 4ab	243	6.00e-64	MG	
			AAL2583 4.1	decay-accelerating factor 3	242	7.00e-64	MG	
	NM_023740 NP_07622 9.1	Mm.20387 F:(C-HI) -1.7, F:(C-D) -2.35, U:(HI-D) 2.52	AAG2376 6.1	PP3774	648	0	MG	
			AAH0807 4.1	Similar to RIKEN cDNA 1500015N03 gene	638	0	MG	
			AAH3315 7.1	similar to Abl-philin 2	523	1.00e-148	MG	

			NP_11570 3.1	hypothetical protein MGC2993	452	1.00e- 127	MG	
5	NM_0097 44 NP_03387 4.1	Mm.15811 F:(C-D) -4.15, U:(HI-D) 2.11	NP_00169 7.2	B-cell lymphoma 6 protein; B-cell CLL/lymphoma-6; cys-his2 zinc finger transcription factor BCL5; zinc finger protein 51; lymphoma-associated zinc finger gene on chromosome 3	133 7	0	MG	
			A48752	B-cell CLL/lymphoma 6 (BCL6) protein	133 0	0	MG	
			BAC0096 2.1	BAZF	335	1.00e- 91	MG	
			XP_17184 9.1	similar to Bcl6-associated zinc finger protein	300	7.00e- 81	MG	
10	NM_0082 45 NP_03227 1.1	Mm.33896 F:(C-D) -2.62, U:(HI-D) 2.05	NP_00272 0.1	hematopoietically expressed homeobox; proline-rich homeodomain-containing transcription factor	381	1.00e- 108	MG	
			JN0767	homeobox protein HEX - human	380	1.00e- 105	MG	
			AAH1433 6.1	Similar to hematopoietically expressed homeobox	379	1.00e- 105	MG	
15			CAA7973 0.1	homeobox related protein	246	2.00e- 65	MG	
	NM_0200 13 NP_06439 7.1	Mm.14373 6 U:(C-HI) 6.00, U:(C-D) 5.03, F:(HI-D) -3.06	AAH1840 4.1	fibroblast growth factor 21	301	3.00e- 81	MG	
20			NP_06198 6.1	fibroblast growth factor 21 precursor	298	5.00e- 80	MG	
	X82786 CAA5802 6.1	Mm.4078 U:(C-HI) 4.07, F:(HI-D) -4.25	NP_00240 8.2	antigen identified by monoclonal antibody Ki-67; Proliferation-related Ki-67 antigen	171 1	0	MG	
25			CAA4652 0.1	antigen of the monoclonal antibody Ki-67	131 5	0	MG	
			B48666	cell proliferation antigen Ki-67, short form - human	127 6	0	MG	
	NM_0100 00 NP_03413 0.1	Mm.876 U:(C-HI) 34.21, U:(C-D) 8.32, F:(HI-D) -3.81	NP_00075 8.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	671	0	MG	
			AAF1360 2.1	cytochrome P450-2B6	665	0	MG	
			NP_00075 7.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	499	1.00e- 140	MG	
			Q16696	Cytochrome P450 2A13 (CYP1A13)	494	1.00e- 138	MG	
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 - human	489	1.00e- 137	MG	
35			CAA3211 7.1	P-450 IIA3 protein (1 is 3rd base in codon)	489	1.00e- 137	MG	

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			NP_00075 3.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	487	1.00e- 136	MG
			CAA3209 7.1	cytochrome P-450IIA (AA 1 - 489)	486	1.00e- 136	MG
			1609083A	cytochrome P450IIA	486	1.00e- 136	MG
			P11509	Cytochrome P450 2A6 (CYP1A6) (Coumarin 7-hydroxylase) (IIA3) (CYP2A3) (P450(I))	486	1.00e- 136	MG
			AAF1360 0.1	cytochrome P450-2A6	485	1.00e- 136	MG
			C34271	cytochrome P450 2A4 - human	485	1.00e- 135	MG
			P20853	Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)	484	1.00e- 135	MG
			NP_00075 5.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 1	483	1.00e- 135	MG
			I38965	cytochrome P450 - human	480	1.00e- 134	MG
			AAA5214 3.1	cytochrome P450-IIB	478	1.00e- 134	MG
			I38967	cytochrome P450 - human	471	1.00e- 131	MG
			AAH2059 6.1	Unknown (protein for MGC:22146)	462	1.00e- 129	MG
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	462	1.00e- 129	MG
			NP_00076 5.2	cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily IIF, polypeptide 1	461	1.00e- 128	MG
			AAA5216 1.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	461	1.00e- 128	MG
			NP_00076 1.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	459	1.00e- 128	MG
			NP_00076 3.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	458	1.00e- 127	MG
			AAA5216 0.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	458	1.00e- 127	MG
			S66382	cytochrome P450 2C8 - human	458	1.00e- 127	MG
			AAB3529 2.1	cytochrome P450 arachidonic acid epoxigenase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	458	1.00e- 127	MG
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	456	1.00e- 127	MG
			AAL6965 2.1	cytochrome P450 2F1	455	1.00e- 126	MG

			BAA0012 3.1	cytochrome P-450	449	1.00e- 125	MG
			NP_00076 2.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	449	1.00e- 125	MG
			AAB2386 4.2	cytochrome P-450	449	1.00e- 125	MG
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	445	1.00e- 123	MG
5			AAA5215 7.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	445	1.00e- 123	MG
			NP_00076 0.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	444	1.00e- 123	MG
10	NM_0096 89 NP_03381 9.1	Mm.8552 U:(C-HI) 3.67, F:(HI-D) -3.5	NP_00115 9.1	baculoviral IAP repeat-containing protein 5; apoptosis inhibitor 4; survivin	258	6.00e- 68	MG
			pdb 1F3H	Survivin; Chain: A, B; Synonym: Apoptosis Inhibitor 4	258	1.00e- 67	MG
			BAA9367 6.1	survivin-beta	245	5.00e- 64	MG
15	NM_0106 34 NP_03476 4.1	Mm.741 U:(C-HI) 3.17, F:(HI-D) -5.62	NP_00143 5.1	fatty acid binding protein 5 (psoriasis-associated); E-FABP	220	2.00e- 56	MG
20	NM_0076 59 NP_03168 5.1	Mm.4761 U:(C-HI) 3.00, F:(HI-D) -2.87	NP_00177 7.1	cell division cycle 2 protein, isoform 1; cell division control protein 2 homolog; cyclin-dependent kinase 1; p34 protein kinase; cell cycle controller CDC2	577	1.00e- 163	MG
			NP_00124 9.1	cyclin-dependent kinase 3	393	1.00e- 108	MG
			CAA4380 7.1	cell division kinase. CDC2 homolog	390	1.00e- 107	MG
			NP_00178 9.2	cyclin-dependent kinase 2, isoform 1; cdc2-related protein kinase; cell division kinase 2; p33 protein kinase	389	1.00e- 107	MG
25			pdb 1E1X	Cyclin-Dependent Protein Kinase 2; Chain: A; Synonym: Cdk2; Ec: 2.7.1.37	389	1.00e- 107	MG
			pdb 1E9H	Cyclin-Dependent Kinase 2, Cdk2; Ec: 2.7.1.37	387	1.00e- 108	MG
			pdb 1GY3	Pcdk2/Cyclin A In Complex With Mgadp, Nitrate and Peptide Substrate	387	1.00e- 106	MG
			CAA4398 5.1	cdk2	387	1.00e- 108	MG
			pdb 1JST	Cyclin-Dependent Kinase-2; Chain: A, C; Synonym: Cdk2; Ec: 2.7.1.-	387	1.00e- 106	MG
30			pdb 1GII	Cell Division Protein Kinase 2; Chain: A; Synonym: Cyclin Dependent Kinase 2; Ec: 2.7.1.37	382	1.00e- 105	MG
			AAH3300 5.1	PCTAIRE protein kinase 2	327	2.00e- 88	MG



			S23384	protein kinase (EC 2.7.1.37) cdc2-related PCTAIRE-2 - human	326	3.00e-88	MG
			NP_002586.1	PCTAIRE protein kinase 2; serine/threonine-protein kinase PCTAIRE-2; protein kinase cdc2-related PCTAIRE-2	324	2.00e-87	MG
			pdj1H4L	Cdk5-P25(Nck5A) Complex - Protein Kinase II Catalytic Subunit, Cdk5 - Cdk5 Activator 1, Cyclin-Dependent Kinase 5 Regulatory Subunit 1, Protein Kinase II 23 Kda Subunit, Tpkii Regulatory Subunit, P23, P25, P35	320	2.00e-86	MG
			NP_004926.1	cyclin-dependent kinase 5	320	2.00e-86	MG
5			JE0374	cyclin-dependent kinase 5 (EC 2.7.-.-) - human	320	2.00e-86	MG
	NM_007822 NP_031848.1	Mm.7459 U:(C-HI) 24.5, F:(C-D) -5.06, F:(HI-D) -7.06	NP_000769.1	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase	780	0	MG
10			Q02928	Cytochrome P450 4A11 precursor (CYPIVA11) (Fatty acid omega-hydroxylase) (P-450 HK omega) (Lauric acid omega-hydroxylase) (CYP4A11) (P450-HL-omega)	777	0	MG
			I65981	fatty acid omega-hydroxylase (EC 1.14.15.-) cytochrome P450 4A11 - human	765	0	MG
			BAA02864.1	fatty acid omega-hydroxylase	761	0	MG
			AAF76722.1	fatty acid omega-hydroxylase CYP4A11	746	0	MG
			CAB72105.1	dJ18D14.4 (cytochrome P450, subfamily IVA, polypeptide 11)	736	0	MG
15			O4HUB1	cytochrome P450 4B1 - human	499	1.00e-139	MG
			AAL57720.1	cytochrome P450	499	1.00e-139	MG
			AAM09532.1	cytochrome P450	499	1.00e-139	MG
			NP_000770.1	cytochrome P450, subfamily IVB, polypeptide 1; cytochrome P450, subfamily IVB, member 1; microsomal monooxygenase	497	1.00e-139	MG
			AAL57721.1	cytochrome P450	497	1.00e-139	MG
20			AAH17758.1	Unknown (protein for MGC:22150)	495	1.00e-138	MG
			AAH28102.1	Unknown (protein for MGC:40051)	489	1.00e-137	MG
			BAC03751.1	unnamed protein product	448	1.00e-124	MG
			BAC04868.1	unnamed protein product	402	1.00e-110	MG
			BAA75823.1	Leukotriene B4 omega-hydroxylase	398	1.00e-109	MG
25			NP_001073.3	tochrome P450, subfamily IVF, polypeptide 2; leukotriene B4 omega-hydroxylase; leukotriene-B4 20-monooxygenase	398	1.00e-109	MG

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			NP_00088 7.1	cytochrome P450, subfamily IVF, polypeptide 3; leukotriene B4 omega hydroxylase; leukotriene-B4 20-monooxygenase; cytochrome P450-LTB-omega	394	1.00e- 108	MG
			AAC5005 2.2	cytochrome P450 4F2	393	1.00e- 108	MG
			AAC0858 9.1	cytochrome P-450	390	1.00e- 107	MG
			Q9HBI6	Cytochrome P450 4F11 (CYPIVF11)	387	1.00e- 106	MG
			NP_06701 0.1	cytochrome P450, subfamily IVF, polypeptide 11	387	1.00e- 106	MG
			Q9HCS2	Cytochrome P450 4F12 (CYPIVF12)	384	1.00e- 105	MG
			NP_07643 3.1	cytochrome P450 isoform 4F12	384	1.00e- 105	MG
			AAH3535 0.1	similar to cytochrome P450	384	1.00e- 105	MG
			AAC1154 3.1	F22329_1	381	1.00e- 104	MG
			NP_00918 4.1	cytochrome P450, subfamily IVF, polypeptide 8; microsomal monooxygenase; flavoprotein-linked monooxygenase	380	1.00e- 104	MG
			CAD3879 5.1	hypothetical protein	347	6.00e- 94	MG
			XP_06506 9.2	similar to CYTOCHROME P450 4F6 (CYPIVF6)	337	6.00e- 91	MG
			XP_02907 0.2	similar to Cytochrome P450 4F12 (CYPIVF12)	323	9.00e- 87	MG
			AAH2285 1.1	Similar to cytochrome P450, subfamily IVA, polypeptide 11	287	6.00e- 76	MG
			XP_06506 8.1	similar to Cytochrome P450 4F12 (CYPIVF12)	278	2.00e- 73	MG
			BAC0502 6.1	unnamed protein product	278	2.00e- 73	MG
			BAA0214 5.1	cytochrome P-450LTBV	270	6.00e- 71	MG
			CAA5058 6.1	cytochrome P450	263	1.00e- 68	MG
			AAL5771 9.1	truncated cytochrome P450	237	5.00e- 61	MG
	NM_0102 86 NP_03441 6.1	Mm.22216 U:(C-HI) 2.83, F:(HI-D) -2.17	Q99576	Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R)	196	8.00e- 49	MG
			T14749	hypothetical protein DKFZp566A093.1 - human	188	2.00e- 46	MG
	NM_0083 62 NP_03238 8.1	Mm.896 U:(C-HI) 2.59, F:(HI-D) -2.22	NP_00086 8.1	Interleukin 1 receptor, type I	823	0	MG
			pdb 1IRA	Interleukin-1 Receptor Antagonist; Chain: X; Synonym: IL1Ra	451	1.00e- 125	MG
			pdb 1ITB	Type-1 Interleukin-1 Receptor Complexed With Interleukin-1 Beta	448	1.00e- 124	MG
			pdb 1GOY	IL-1 Receptor Type 1 Complexed With Antagonist Peptide Af10847	445	1.00e- 123	MG

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			XP_00268 5.3	similar to IL-1Rrp2	562	2.00e- 96	MG
			AAG2136 8.1	IL-1Rrp2	356	2.00e- 96	MG
			NP_00384 5.1	interleukin 1 receptor-like 2	354	7.00e- 96	MG
			NP_05731 6.2	Interleukin 1 receptor-like 1; interleukin 1 receptor 1; ST2V protein	208	5.00e- 52	MG
			NP_05911 2.1	Interleukin 1 receptor accessory protein-like 2	206	3.00e- 51	MG
			AAF5941 2.1	X-linked interleukin-1 receptor accessory protein-like 2	206	3.00e- 51	MG
NM_0105 44 NP_03467 4.1	Mm.2543	U:(C-HI) 2.45, F:(HI-D) -2.47	Q14623	Indian hedgehog protein precursor (IHH) (HHG-2)	725	0	MG
			AAA6217 8.1	indian hedgehog protein	612	1.00e- 174	MG
			XP_05084 6.2	similar to Indian hedgehog protein precursor (IHH) (HHG-2)	578	1.00e- 183	MG
			2117287B	Indian hedgehog gene	553	1.00e- 156	MG
			NP_00018 4.1	sonic hedgehog preproprotein	451	1.00e- 125	MG
			NP_06638 2.1	desert hedgehog preproprotein	428	1.00e- 118	MG
			2117287A	Sonic hedgehog gene	420	1.00e- 116	MG
			AAB6760 4.1	Sonic Hedgehog; associated with holoprosencephaly in humans and segment polarity defects in Drosophila	296	8.00e- 79	MG
NM_0118 19 NP_03594 9.1	Mm.31325	U:(C-HI) 2.39, U:(C-D) 2.00, F:(HI-D) -2.52	JCS697	placental transforming growth factor-beta homolog - human	284	2.00e- 75	MG
			AAC3953 7.1	prepro placental TGF-beta	281	1.00e- 74	MG
			XP_03809 8.1	similar to Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)...	281	1.00e- 74	MG
			AAC2445 6.1	prostate differentiation factor	281	1.00e- 74	MG
			Q99988	Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)	281	2.00e- 74	MG
			NP_00485 5.1	ate differentiation factor; PTGF-beta	280	5.00e- 74	MG
NM_0196 41 NP_06261 5.1	Mm.28479	U:(C-HI) 2.29, F:(HI-D) -2.08	NP_00555 4.1	stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; stathmin; leukemia-associated phosphoprotein p18	286	6.00e- 77	MG

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			AAH1435 3.1	Similar to stathmin 1/oncoprotein 18	285	2.00e- 76	MG
NM_0101 21 NP_03425 1.1	Mm.23375	U:(C-HI) 2.15, F:(HI-D) -2.19	Q9NZJ5	Eukaryotic translation initiation factor 2-alpha kinase 3 precursor (PRKR-like endoplasmic reticulum kinase) (Pancreatic eIF2-alpha kinase) (HsPEK)	175 9	0	MG
			NP_00482 7.2	eukaryotic translation initiation factor 2-alpha kinase 3; eukaryotic translation initiation factor 2 alpha kinase 3	175 7	0	MG
NM_0113 18 NP_03544 8.1	Mm.2165	U:(C-HI) 2.03, F:(HI-D) -2.37	AAA6030 2.1	pre-serum amyloid P component	316	3.00e- 85	MG
			NP_00163 0.1	serum amyloid P component precursor; amyloid P component, serum; pentaxin-related; 9.5S alpha-1-glycoprotein	316	3.00e- 85	MG
			pdbs1SAC	Serum Amyloid P Component (Sap)	296	2.00e- 79	MG
			XP_04967 3.1	similar to C-reactive protein precursor	233	2.00e- 60	MG
			pdbs1IJ7	C-Reactive Protein; Chain: A, B, C, D, E, F, G, H, I, J	223	2.00e- 57	MG
			NP_00055 8.1	C-reactive protein, pentraxin-related; C-reactive protein	214	2.00e- 54	MG
NM_0168 47 NP_05854 3.1	Mm.4351	U:(C-HI) 2.02, F:(HI-D) -2.03	NP_00069 7.1	arginine vasopressin receptor 1A; V1a vasopressin receptor; vascular/hepatic-type arginine vasopressin receptor; antidiuretic hormone receptor 1A	701	0	MG
			NP_00069 8.1	arginine vasopressin receptor 1B; arginine vasopressin receptor 3; antidiuretic hormone receptor 1B; vasopressin V1B receptor; pituitary vasopressin receptor 3	364	4.00e- 99	MG
			NP_00090 7.1	oxytocin receptor	355	2.00e- 96	MG
			1808301A	oxytocin receptor	355	2.00e- 96	MG
			CAA5656 2.1	oxytocin receptor	299	1.00e- 79	MG
			NP_00004 5.1	arginine vasopressin receptor 2	244	5.00e- 63	MG
			1913493A	vasopressin receptor:ISOTYPE=V2	241	3.00e- 62	MG
			AAB8767 8.1	vasopressin receptor type 2	216	1.00e- 54	MG
NM_0113 69 NP_0354 99.1	Mm.3780 1	U:(C-IR)+2. 13 F:(IR-D)-2.5 3	NP_07902 1	likely ortholog of mouse Shc SH2-domain binding protein 1; hypothetical protein FLJ22009	100 4	0	
			BAB7104 9.	unnamed protein product	100 3	0	
			BAB1520 8	unnamed protein product	630	1.00e- 180	
			AAH0096 0	Unknown (protein for IMAGE:3451160)	615	1.00e- 176	
			AAG4533 6	GE36	230	7.00e- 60	
			NP_11219 5	chromosome 1 open reading frame 14; GE36 gene	228	2.00e- 59	

			AAG6061			5.00e-
			6	C1orf14	204	52

**Master Table 2 - Human Protein Classes**  
**Subtable 2A: Favorable**

	Mouse	Behavi	Human Protein Class
5	NM_007630 NP_031656.1	F:(HI-D) -5.28	Cyclin Subclass: cyclin B2 Subclass: cyclin B1; G2/mitotic-specific cyclin B1
10	NM_007913 NP_031939.1	F:(HI-D) -2.66	Early growth response Subclass: early growth response 1; G0S30 Subclass: early growth response 3
15	AF127033 AAG02285.1	F:(HI-D) -2.1	fatty acid synthase; FAS [Homo sapiens]
20	NM_011169 NP_035299.1	F:(HI-D) -2.08	prolactin receptor Subclass: prolactin receptor Subclass: prolactin receptor isoform delta S1 precursor Subclass: prolactin receptor short isoform 1a Subclass: intermediate prolactin receptor isoform
25	AF047725 AAD13720.1	F:(HI-D) -2.06	cytochrome P450, subfamily IIC Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase) Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)

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NM_013490 NP_038518.1	F:(HI-D) -2.04	choline kinase
		Subclass: choline kinase
		Subclass: choline/ethanolamine kinase isoform a
NM_013888 NP_038916.1	F:(HI-D) -2.04	J domain containing protein 1
NM_019499 NP_062372.1	F:(HI-D) -2.04	MAD2-like 1; MAD2 (mitotic arrest deficient, yeast, homolog)-like 1; mitotic arrest deficient, yeast, homolog-like 1
NM_011850 NP_035980.1	F:(HI-D) -2.03	short heterodimer partner; orphan nuclear receptor SHP; small heterodimer partner; nuclear receptor subfamily 0, group B, member 2
AF213393 AAF31432.1	F:(HI-D) -2.02	ATP-binding cassette, sub-family A
		Subclass: ATP-binding cassette, sub-family A member 8
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 9
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 10
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 6
NM_013646 NP_038674.1	F:(HI-D) -2.02	RAR-related orphan receptor
		Subclass: RAR-related orphan receptor A, isoform a; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform c; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform b; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform d; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor B; RAR-related orphan receptor beta; retinoic acid-binding receptor beta; nuclear receptor RZR-beta
NM_009425 NP_033451.1	F:(HI-D) -10.21	tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related apoptosis inducing ligand TRAIL
NM_008182 NP_032208.1	F:(C-HI) -9.17, F:(C-D) -5.68	glutathione transferase

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		Subclass: glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2
		Subclass: TPA: glutathione transferase A5
		Subclass: Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)
		Subclass: Glutathione S-transferase A3-3 (GST class-alpha)
		Subclass: glutathione S-transferase A3
		Subclass: glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human
NM_028089 NP_082365.1	F:(C-HI) -4.31, F:(C-D) -5.26	cytochrome P-450
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
		Subclass: cytochrome P450 2C17
NM_007818 NP_031844.1	F:(C-HI) -4.29, F:(C-D) -8.15	cytochrome P450
		Subclass: Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP11A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3



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		Subclass: cytochrome P450, subfamily IIIA, polypeptide 5; niphedipine oxidase; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 7; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450 polypeptide 43 isoform 2; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 1; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 3; cytochrome P450 polypeptide 43
NM_025429 NP_079705.1	F:(C-HI) -3.51, F:(C-D) -3.01	serine (or cysteine) proteinase inhibitor
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)
NM_008341 NP_032367.1	F:(C-HI) -3.37, F:(C-D) -3.47, F:(HI-D) -2.63	insulin-like growth factor binding protein 1
NM_009669 NP_033799.1	F:(C-HI) -3.13	Alpha-Amylase
		Subclass: amylase, alpha 2A; pancreatic; Amylase, pancreatic, alpha-2A
		Subclass: amylase, alpha 2B; pancreatic; Amylase, pancreatic, alpha-2B

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		Subclass: similar to Alpha-amylase, salivary precursor (1,4-alpha-D-glucan glucanohydrolase)
		Subclass: amylase, alpha 1A; salivary; Amylase, salivary, alpha-1A
5	U38940 AAA85125.1	F:(C-HI) -3.11, F:(C-D) -2.11  asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein
	J03953 AAA37748.1	F:(C-HI) -3.03  Chain A, ligand-free Glutathione S-Transferase
10		Subclass: Chain A, ligand-free, Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase Mu 4
		Subclass: Chain A, glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-aralkyltransferase M2
		Subclass: Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)
		Subclass: Similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)
15	NM_013459 NP_038487.1	F:(C-HI) -2.94  Complement factor D
		Subclass: Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)
		Subclass: Chain , Mutant Of Factor D With Enhanced Catalytic Activity
		Subclass: Chain , Human Complement Factor D In Complex With Isatoic Anhydride Inhibitor
20	NM_016810 NP_058090.1	F:(C-HI) -2.86  golgi SNAP receptor complex member 1; Golgi SNARE 28 kDa
25	AK006128 BAB24422.1	F:(C-HI) -2.71  ATP-binding cassette
		Subclass: ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter
		Subclass: multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2)

		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 4; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 3; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 1; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 2; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
5		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 7; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 6; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
	NM_008742 NP_032768.1	F:(C-HI) -2.68 neurotrophin 3
10		
	NM_008361 NP_032387.1	F:(C-HI) -2.65, F:(C-D) -2.03 interleukin 1, beta
	AF294617 AAG02118.1	F:(C-HI) -2.63 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase
15		
	NM_009998 NP_034128.1	F:(C-HI) -2.61, F:(C-D) -2.33 cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6
20	NM_008988 NP_033014.1	F:(C-HI) -2.6 putative neuronal cell adhesion molecule (punc)
		Subclass: putative neuronal cell adhesion molecule (punc)
		Subclass: similar to punc
25	NM_010166 NP_034296.1	F:(C-HI) -2.57 Eyes absent homolog
		Subclass: Eyes absent homolog 3 (EYA3)
		Subclass: eyes absent homolog 4 (Drosophila);
		Subclass: eyes absent 1 isoform b; Eyes absent, Drosophila, homolog of, 1; Melnick-Fraser syndrome

		Subclass: EYA1A	
		Subclass: Eyes absent homolog 2	
		Subclass: EYA1D	
5	AK002480 NP_666065.1	F:(C-HI) -2.55, F:(C-D) -2.57	cystathionase isoform 1; cystathionine gamma-lyase; homoserine deaminase; homoserine dehydratase; cysteine desulphydrase
	AK018226 XP_110043.1	F:(C-HI) -2.53, F:(C-D) -2.4	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin)
10			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)
15	NM_010361 NP_034491.1	F:(C-HI) -2.46, F:(C-D) -2.25	glutathione S-transferase
			Subclass: glutathione S-transferase theta 2
			Subclass: glutathione S-transferase theta 1
20	AK018485 BAB31233.1	F:(C-HI) -2.46	similar to data source:SPTR, source key:Q60928, evidence:ISS~putative~similar to GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE) (GGT)
			Alternate: hypothetical protein FLJ90165
25	NM_010924 NP_035054.1	F:(C-HI) -2.45, F:(C-D) -2.19	nicotinamide N-methyltransferase

5	NM_021307 NP_067282.1	F:(C-HI) -2.44	Zinc finger protein
			Subclass: zinc finger protein 228
			Subclass: similar to ZNF228 protein
			Subclass: Zinc finger protein 226
			Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)
			Subclass: Hypothetical zinc finger-like protein
			Subclass: similar to Zinc finger protein 229
10			Subclass: Zinc finger protein ZNF45
15	NM_008295 NP_032321.1	F:(C-HI) -2.43, F:(C-D) -5.64, F:(HI-D) -2.32	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1; Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid
	NM_010001 NP_034131.1	F:(C-HI) -2.43, F:(C-D) -2.56	cytochrome P450
			Subclass: Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)
			Subclass: cytochrome P450 2C19
20			Subclass: cytochrome P450 2C9
			Subclass: cytochrome P450 2C10
			Subclass: cytochrome P450 2C8
25	AK012213 BAB28101.1	F:(C-HI) -2.39, F:(C-D) -2.05	aldehyde dehydrogenase 1 family
			Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5
			Subclass: Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)
			Subclass: Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)
			Subclass: Aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
			Subclass: Aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6

	NM_023154 NP_075643.1	F:(C-HI) -2.39, F:(C-D) -2.48	Similar to RIKEN cDNA 0610025L15 gene product
5	NM_010401 NP_034531.1	F:(C-HI) -2.39, F:(C-D) -2.21	histidine ammonia-lyase; Histidine ammonia-lyase (histidase)
	NM_023455 NP_075944.1	F:(C-HI) -2.39, F:(C-D) -2.04	putative N-acetyltransferase Camello 2
10			Alternate: N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
			Alternate: GLA
			Alternate: kidney- and liver-specific gene product
			Alternate: hypothetical protein TSC501
15	NM_018779 NP_061249.1	F:(C-HI) -2.35, F:(C-D) -2.43	phosphodiesterase
			Subclass: phosphodiesterase 3A, cGMP-inhibited
			Subclass: phosphodiesterase 3B, cGMP-inhibited
20	AK009563 BAB26361.1	F:(C-HI) -2.33	similar to RIKEN cDNA 2310032D16
			Alternate: KIAA1434 protein
	NM_009466 NP_033492.1	F:(C-HI) -2.32, F:(C-D) -2.00	UDP-glucose dehydrogenase (uridine diphosphoglucose dehydrogenase)
25	NM_013584 NP_038612.1	F:(C-HI) -2.31, F:(C-D) -2.46	leukemia inhibitory factor receptor, LIF receptor [human, placenta, Peptide, 1078 aa]
	NM_008061 NP_032087.1	F:(C-HI) -2.28, F:(C-D) -2.14	glucose-6-phosphatase, catalytic
30			

5	NM_025631 NP_079907.1	F:(C-HI) -2.25, F:(C-D) -2.16	hypothetical protein dJ726C3.2
10	NM_025404 NP_079680.1	F:(C-HI) -2.24, F:(C-D) -2.03	ADP-ribosylation factor
			Subclass: ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6
			Subclass: similar to ADP-ribosylation-like 4
			Subclass: ADP-ribosylation factor-like 7
			Subclass: ADP ribosylation factor-like protein
15	NM_008615 NP_032641.1	F:(C-HI) -2.22	NADP-dependent malic enzyme
			Subclass: cytosolic malic enzyme 1; malic enzyme, cytoplasmic; malic enzyme 1, soluble; NADP-dependent malic enzyme; malate dehydrogenase; pyruvic-malic carboxylase
			Subclass: malic enzyme 3, NADP(+)-dependent, mitochondrial; malic enzyme, NADP+-dependent, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase; NADP-ME
			Subclass: malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochondrial; malic enzyme 2, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase
20	NM_026104 NP_080380.1	F:(C-HI) -2.22	similar to RIKEN cDNA 1700095F04 gene product
			Alternate: unnamed protein product
25	NM_008792 NP_032818.1	F:(C-HI) -2.19	proprotein convertase
			Subclass: proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5
			Subclass: proprotein convertase subtilisin/kexin type 1 preproprotein; prohormone convertase 3; prohormone convertase 1; neuroendocrine convertase 1; proprotein convertase 1
30	NM_013743 NP_038771.1	F:(C-HI) -2.19	pyruvate dehydrogenase kinase
			Subclass: pyruvate dehydrogenase kinase, isoenzyme 4
			Subclass: pyruvate dehydrogenase kinase, isoenzyme 1
			Subclass: pyruvate dehydrogenase kinase, isoenzyme 2
			Subclass: pyruvate dehydrogenase kinase, isoenzyme 3

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NM_010357 NP_034487.1	F:(C-HI) -2.17, F:(C-D) -2.93	Glutathione S-transferase Subclass: Glutathione S-transferase A3-3 (GST class-alpha) Subclass: glutathione S-transferase A3 Subclass: glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-aralkyltransferase A1; GST-epsilon; glutathione S-transferase 2 Subclass: glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-aralkyltransferase A2; GST-gamma; HA subunit 2 Subclass: Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k) Subclass: TPA: glutathione transferase A5 Subclass: glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-aralkyltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4
NM_011146 NP_035276.1	F:(C-HI) -2.17	peroxisome proliferative activated receptor gamma peroxisome proliferative activated receptor gamma, isoform 2; PPAR-gamma; peroxisome proliferator activated receptor gamma peroxisome proliferative activated receptor gamma, isoform 1; PPAR-gamma; peroxisome proliferator activated receptor gamma
NM_007395 NP_031421.1	F:(C-HI) -2.16	activin A type IB receptor Subclass: activin A type IB receptor precursor; serine(threonine) protein kinase Subclass: activin A type IB receptor, isoform b precursor; serine(threonine) protein kinase Subclass: activin type I receptor SKR2, splice form 2 Subclass: activin A type IB receptor, isoform c precursor; serine(threonine) protein kinase Subclass: activin type I receptor SKR2 splice form 3 Subclass: transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa); transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kD)

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	NM_009127 NP_033153.1	F:(C-HI) -2.15, F:(C-D) -3.29, F:(HI-D) -2.71	Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)
5	NM_007824 NP_031850.1	F:(C-HI) -2.14, F:(C-D) -3.09	Cytochrome P450 Subclass: Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase) Subclass: cytochrome P450, subfamily VIIIB, polypeptide 1; 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha- Subclass: sterol 12-alpha hydroxylase.CYP8B1
10	AK002979 BAB22492.1	F:(C-HI) -2.14, F:(C-D) -2.15	calcyon
	NM_011817 NP_035947.1	F:(C-HI) -2.13	growth arrest and DNA damage inducible protein gamma (GADD45-gamma)
15	NM_027000 NP_081276.1	F:(C-HI) -2.13	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB) Alternate: G protein-binding protein CRFG; GTP-binding protein Alternate: G protein-binding protein CRFG Alternate: putative G-binding protein Alternate: unnamed protein product
20	NM_007815 NP_031841.1	F:(C-HI) -2.11, F:(C-D) -2.78	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), Subclass: Cytochrome P450 2C18 (CYP1IC18) (P450-6B/29C) Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
25			

		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17	
		Subclass: cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1'	
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	
5	AK006487 BAB24612.1	F:(C-HI) -2.1	hypothetical protein BC015148
	NM_008587 NP_032613.1	F:(C-HI) -2.1	c-mer proto-oncogene tyrosine kinase
10	NM_007912 NP_031938.1	F:(C-HI) -2.09, F:(C-D) -2.69	Epidermal growth factor receptor
			Subclass: epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian); epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Epidermal growth factor receptor
			Subclass: p110 epidermal growth factor receptor
15			Subclass: v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4
			Subclass: v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian); Transformation gene ERBB-3; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
			Subclass: Receptor protein-tyrosine kinase erbB-3 (c-erbB3) (Tyrosine kinase-type cell surface receptor HER3)
			Subclass: v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog; Avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 2; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)
			Subclass: Similar to v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
20			Subclass: herstatin
	NM_010145 NP_034275.1	F:(C-HI) -2.09, F:(C-D) -2.09	epoxide hydrolase 1, microsomal (xenobiotic); Epoxide hydroxylase 1, microsomal (xenobiotic)
25	NM_009676 NP_033806.1	F:(C-HI) -2.08	aldehyde oxidase 1

	NM_010012 NP_034142.1	F:(C-HI) -2.08	cytochrome P450, subfamily VIIB, polypeptide 1 (CYP8B1); 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-hydroxylase
5	NM_011921 NP_036051.1	F:(C-HI) -2.08	aldehyde dehydrogenase 1
			Subclass: aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
			Subclass: aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2
10			Subclass: aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6
			Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5
	NM_018776 NP_061246.1	F:(C-HI) -2.07, F:(C-D) -2.11	cytokine receptor related protein
15			Subclass: cytokine receptor related protein 4
			Subclass: cytokine receptor-like factor 3
			Subclass: cytokine receptor-like molecule 9
	NM_007474 NP_031500.1	F:(C-HI) -2.07	aquaporin 8
20	NM_023737 NP_076226.1	F:(C-HI) -2.07	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
	AK005535 BAB24106.1	F:(C-HI) -2.06, F:(C-D) -2.16	solute carrier family 39 (zinc transporter), member 4
25	NM_009864 NP_033994.1	F:(C-HI) -2.05	Cadherin
			Subclass: cadherin 1, type 1 preproprotein; calcium-dependent adhesion protein, epithelial; cadherin 1, E-cadherin (epithelial); uvomorulin; cell-CAM 120/80; Arc-1
30			Subclass: E-cadherin
			Subclass: cadherin 3, type 1 preproprotein; P-cadherin; placental cadherin; cadherin 3, P-cadherin (placental); calcium-dependent adhesion protein, placental
			Subclass: cadherin 2, type 1 preproprotein; N-cadherin 1; cadherin 2, N-cadherin (neuronal); neural cadherin; calcium-dependent adhesion protein, neuronal

		Subclass: cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-cadherin; retinal cadherin
		Subclass: Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-CAD)
		Alternate: uvomorulin
5	NM_023341 NP_075830.1	F:(C-HI) -2.05 chaperone
		Subclass: chaperone-ABC1-like
		Subclass: chaperone, ABC1 activity of bc1 complex like
10		Alternate: unnamed protein product
	AF071068 AAC25566.1	F:(C-HI) -2.04, F:(C-D) -2.29 decarboxylase
		Subclass: dopa decarboxylase (aromatic L-amino acid decarboxylase); aromatic L-amino acid decarboxylase
15		Subclass: Histidine decarboxylase (HDC)
	NM_009263 NP_033289.1	F:(C-HI) -2.04 Osteopontin
		Subclass: Osteopontin precursor (Bone sialoprotein 1) (Urinary stone protein) (Secreted phosphoprotein 1) (SPP-1) (Nephropontin) (Uropontin)
20		Subclass: OPN-a
		Subclass: OPN-b
		Subclass: OPN-c
25	NM_053200 NP_444430.1	F:(C-HI) -2.04 carboxylesterase
		Subclass: carboxylesterase 3; brain carboxylesterase BR3
		Subclass: brain carboxylesterase hBr2
		Subclass: carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)
		Subclass: Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)
30		Subclass: serine esterase N-terminal truncated (503 AA)
		Subclass: brain carboxylesterase hBr1
		Subclass: Alternate: acyl coenzyme A:cholesterol acyltransferase
	AK007964 BAB25375.1	F:(C-HI) -2.03, F:(C-D) -2.36 cholinephosphotransferase 1

	NM_009748 NP_033878.1	F:(C-HI) -2.03, F:(C-D) -2.15	Golgi vesicular membrane trafficking protein p18; Bet1 (S. cerevisiae) homolog; Bet1p homolog
5	NM_019811 NP_062785.1	F:(C-HI) -2.03, F:(C-D) -2.11	acetyl-CoA synthetase
			Subclass: acetyl-CoA synthetase isoform a; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
			Subclass: acetyl-CoA synthetase isoform b; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
10	NM_011834 NP_035964.1	F:(C-HI) -2.03	L-kynurenine/alpha-aminoadipate aminotransferase; kynurenine aminotransferase II
			Alternate: Similar to L-kynurenine/alpha-aminoadipate aminotransferase
15	NM_009221 NP_033247.1	F:(C-HI) -2.02	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor
	NM_011125 NP_035255.1	F:(C-HI) -2.01	phospholipid transfer protein
			Alternate: Similar to phospholipid transfer protein
20	NM_010062 NP_034192.1	F:(C-HI) -2.00, F:(C-D) -2.4	deoxyribonuclease
			Subclass: deoxyribonuclease II, lysosomal; DNase II, lysosomal
		-	Subclass: deoxyribonuclease II beta, isoform 1 precursor; DNase II-like acid DNase; endonuclease DLAD
25	NM_007811 NP_031837.1	F:(C-HI) -17.03, F:(C-D) -3.81	Cytochrome P450 26 (Retinoic acid-metabolizing cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase)
	NM_053215 NP_444445.1	F:(C-HI) -1.98, F:(C-D) -3.23	UDP glycosyltransferase; UDP-glucuronyltransferase

		Subclass: UDP glycosyltransferase 2 family, polypeptide B17; UDP-glucuronyltransferase, family 2, beta-17	
		Subclass: similar to UDP-glucuronosyltransferase 2B15 precursor, microsomal (UDPGT) (UDPGTH-3) (HLUG4)	
		Subclass: UDP glycosyltransferase 2 family, polypeptide B15; UDP-glucuronyltransferase, family 2, beta-15	
		Subclass: UDP glycosyltransferase 2 family, polypeptide B4; UDP-glucuronyltransferase, family 2, beta-4	
5		Subclass: similar to UDP-glucuronosyltransferase 2B4 precursor, microsomal (UDPGT) (Hyodeoxycholic acid) (HLUG25) (UDPGTH-1)	
		Subclass: UDP glycosyltransferase 2 family, polypeptide B7; UDP-glucuronyltransferase, family 2, beta-7	
		Subclass: UDP glycosyltransferase 2 family, polypeptide A1; UDP glucuronosyltransferase 2 family, polypeptide A1	
		Subclass: UDP glycosyltransferase 2 family, polypeptide B11	
		Subclass: UDP glycosyltransferase 2 family, polypeptide B10	
10		Subclass: UDP glycosyltransferase 2 family, polypeptide B28	
	NM_009993 NP_034123.1	F:(C-D) -3.27	cytochrome P450
			Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase
15			Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase
			Subclass: cytochrome P450 CYP1B1
	NM_007706 NP_031732.1	F:(C-D) -2.51	suppressor of cytokine signaling-2; STAT induced STAT inhibitor-2; cytokine-inducible SH2 protein 2
20			
	NM_009396 NP_033422.1	F:(C-D) -2.5	tumor necrosis factor, alpha-induced protein 2
	AK004924 BAB23675.1	F:(C-D) -2.42	similar to coenzyme A diphosphatase
25	NM_029813 NP_084089.1	F:(C-D) -2.4	zinc finger protein
			Subclass: zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
			Subclass: similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
			Subclass: similar to zinc finger protein 91 (HPF7, HTF10)
30			Subclass: zinc finger protein 180 (HHZ168)

		Subclass: zinc finger protein 136 (clone pHZ-20)
		Subclass: KIAA1710 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1710
5		Subclass: Zinc finger protein 93 (Zinc finger protein HTF34)
		Subclass: zinc finger protein 135 (clone pHZ-17)
		Subclass: zinc finger protein 85 (HPF4, HTF1)
		Subclass: KIAA1198 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1198
10		Subclass: similar to Zinc finger protein 135
		Subclass: similar to Zinc finger protein 93 (Zinc finger protein HTF34)
		Subclass: zinc finger protein 91 (HPF7, HTF10)
		Subclass: zinc finger protein 84 (HPF2)
		Subclass: finger protein 2, placental
15		similar to KRAB zinc finger protein KR18
		Subclass: zinc finger protein AF020591
		Subclass: kruppel-related zinc finger protein
		Subclass: Similar to zinc finger protein 208
		Subclass: zinc finger protein 71; endothelial zinc finger protein induced by tumor necrosis factor alpha
		Subclass: zinc finger protein 37 homolog (mouse); Zinc finger protein-37, mouse, homolog of; zinc finger protein homologous to Zfp37 in mouse
20		Subclass: zinc finger protein 328
		Subclass: similar to zinc finger protein 29
		Subclass: zinc finger protein 268
		Similar to zinc finger protein 208
		Subclass: Zinc finger protein ZNF45
25		Subclass: zinc finger protein 16 (KOX 9)
		Subclass: similar to Zinc finger protein 85
		Subclass: zinc finger protein 43 (HTF6)
		Subclass: similar to Zinc finger protein 35 (Zfp-35)
		Subclass: zinc finger protein 228
30		Subclass: similar to Zinc finger protein 20 (Zinc finger protein KOX13)
		Subclass: similar to Zinc finger protein 184
		Subclass: zinc finger protein 177
		Subclass: bB479F17.3 (zinc finger protein 41)
		Subclass: similar to Zinc finger protein 41
35		Subclass: zinc finger protein 287
		Subclass: zinc finger protein 331; zinc finger protein 463; C2H2-like
		Subclass: zinc finger protein 271
		Subclass: Hypothetical zinc finger protein KIAA1473
		Subclass: similar to Hypothetical zinc finger protein KIAA1473
40		Subclass: similar to Hypothetical zinc finger protein KIAA1956
		Subclass: KRAB zinc finger protein
		Subclass: KIAA1956 protein

		Subclass: TRAF6-inhibitory zinc finger protein; TRAF6-binding zinc finger protein
		Alternate: hypothetical protein
		Subclass: FLJ40981
5		Subclass: similar to hypothetical protein FLJ40981
		Subclass: hypothetical protein FLJ21628
		Subclass: hypothetical protein FLJ32191
		Subclass: hypothetical protein DKFZp572C163.1
		Subclass: hypothetical protein FLJ30932
		Subclass: hypothetical protein FLJ14345
10		Subclass: hypothetical protein FLJ90396
		Subclass: hypothetical protein FLJ31526
		Subclass: hypothetical protein DKFZp572P0920.1
15	NM_007494 NP_031520.1	F:(C-D) -2.36 argininosuccinate synthetase
		Subclass: argininosuccinate synthetase
		Subclass: similar to argininosuccinate synthetase
20	NM_008792 NP_032818.1	F:(C-D) -2.35 proprotein convertase subtilisin/kexin type 2; subtilisin-like proenzyme convertases; proenzyme convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5
	AK010786 BAB27182.1	F:(C-D) -2.27 tubulin, beta polypeptide
25		Subclass: tubulin, beta, 2
		Subclass: tubulin, beta, 4 (tubulin beta-III)
		Subclass: tubulin, beta, 5
		Subclass: tubulin beta-1
		Subclass: similar to tubulin, beta 3
		Subclass: tubulin, beta polypeptide 4, member Q
30		Subclass: beta tubulin 1, class VI
		Subclass: similar to beta-tubulin 4Q
		Alternative: similar to neu differentiation factor - human (fragment)
35	NM_008183 NP_032209.1	F:(C-D) -2.27 Glutathione S-transferase
		Subclass: similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: glutathione transferase M1
		Subclass: glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2



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		Subclass: glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-aralkyltransferase M5; GST class-mu 5
		Subclass: glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-aralkyltransferase M4; GTS-Mu2; GST class-mu 4
		Subclass: glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-aralkyltransferase M4; GTS-Mu2; GST class-mu 4
		Subclass: Similar to glutathione S-transferase M2 (muscle)
		Subclass: similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)
		Subclass: Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form
		Subclass: glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human
		Subclass: glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-aralkyltransferase; GST class-mu
NM_012006 NP_036136.1	F:(C-D) -2.24	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)
		Alternate: peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein
		Alternate: Similar to peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein
AK006569 BAB24656.1	F:(C-D) -2.18	hypothetical protein FLJ20456
		Alternative: Unknown (protein for MGC:21737)
NM_010107 NP_034237.1	F:(C-D) -2.18	ephrin-A1
NM_025754 NP_080030.1	F:(C-D) -2.13	aldolase
		Subclass: Aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase
		Subclass: aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase
NM_008303 NP_032329.1	F:(C-D) -2.12	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (chaperonin 10)

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NM_011300 NP_035430.1	F:(C-D) -2.11	ribosomal protein
		Subclass: ribosomal protein S7; 40S ribosomal protein S7
		Subclass: similar to ribosomal protein S7
AK011896 BAB27902.1	F:(C-D) -2.1	unnamed protein product
NM_008322 NP_032348.1	F:(C-D) -2.1	isocitrate dehydrogenase 2 (NADP+), mitochondrial; Isocitrate dehydrogenase, mitochondrial
NM_011802 NP_035932.1	F:(C-D) -2.08	ClpX caseinolytic protease X homolog; energy-dependent regulator of proteolysis; ClpX (caseinolytic protease X, E. coli)
AK004138 BAB23187.1	F:(C-D) -2.06	ORFII
		Alternative: hypothetical protein FLJ20048
		Alternative: putative p150
NM_008509 NP_032535.1	F:(C-D) -2.05, F:(HI-D) -2.42	lipoprotein lipase
		Subclass: lipoprotein lipase precursor
		Subclass: Similar to lipoprotein lipase
		Subclass: lipoprotein lipase
NM_013541 NP_038569.1	F:(C-D) -2.05	glutathione S-transferase
		Subclass: glutathione transferase pi
		Subclass: glutathione S-transferase-P1c
		Subclass: Chain A, Glutathione S-Transferase P1-1
		Subclass: glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester synthase III
NM_008756 NP_032782.1	F:(C-D) -2.04	occludin
NM_009349 NP_033375.1	F:(C-D) -2.04	Methyltransferase
		Subclass: Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)
		Subclass: indolethylamine N-methyltransferase; thioester S-methyltransferase-like

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		Subclass: thioether S-methyltransferase-like; similar to P40936 (PID:g731019)
		Subclass: nicotinamide N-methyltransferase
5	NM_023850 NP_076339.1	F:(C-D) -2.03 carbohydrate sulfotransferase
		Subclass: carbohydrate (keratan sulfate Gal-6) sulfotransferase 1; carbohydrate (chondroitin 6/keratan) sulfotransferase 1
		Subclass: carbohydrate (chondroitin 6) sulfotransferase 3; chondroitin 6-sulfotransferase
		Subclass: carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6; macular dystrophy, corneal, 1; carbohydrate sulfotransferase 6; corneal N-acetylglucosamine 6-sulfotransferase
		Subclass: carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4; N-acetylglucosamine 6-O-sulfotransferase
10	NM_033146 NP_149158.1	F:(C-D) -2.03 Protein CGI-112
		Alternate: similar to Protein CGI-112
15	NM_010324 NP_034454.1	F:(C-D) -2.01 aspartate aminotransferase
		Subclass: aspartate aminotransferase 1; glutamic-oxaloacetic transaminase 1, soluble
		Subclass: glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
20	NM_016978 NP_058674.1	F:(C-D) -2.01 Ornithine aminotransferase
	NM_011172 NP_035302.1	F:(C-D) -2 proline dehydrogenase (oxidase) 1; proline oxidase 2; p53 induced protein
25	NM_013809 NP_038837.1	F:(C-D) -2 cytochrome P450
		Subclass: Cytochrome P450 2A13 (CYP11A13)
		Subclass: coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 -
		Subclass: Cytochrome P450 2A7 (CYP11A7) (P450-IIA4)
30		Subclass: cytochrome P450 2A4 - human
		Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
		Subclass: cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily IIF, polypeptide 1 (H. sapiens)
		Subclass: cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6

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		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYPIIC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYPIIC8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
		Subclass: cytochrome P450, subfamily IIE, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)
		Subclass: cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P540, subfamily IIS, polypeptide 1
		Subclass: cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase; Cytochrome P450, subfamily IIJ (arachidonic acid epoxidase),
		Subclass: cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C17
		Subclass: Cytochrome P450 2C18 (CYPIIC18) (P450-6B/29C)
NM_008184 NP_032210.1	F:(C-D) -1.78	glutathione transferase
		Subclass: Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2
		Subclass: glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4

		Subclass: glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-aralkyltransferase M5; GST class-mu 5	
		Subclass: glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human	
5	AK003797 BAB23001.1	F:(C-D) -1.71	molybdenum cofactor sulfurase
			Alternate: Similar to molybdenum cofactor sulfurase
10	S80191 AAB21335.1	F:(C-D) -1.61	Unknown (protein for MGC:9220)
			Alternate: carboxylesterase
			Subclass: carboxylesterase 1(monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)
			Subclass: acyl coenzyme A:cholesterol acyltransferase
			Subclass: brain carboxylesterase hBr1
15			Subclass: brain carboxylesterase hBr2
			Subclass: egasyn
			Subclass: Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)
			Subclass: carboxylesterase 3; brain carboxylesterase BR3
			Subclass: serine esterase N-terminal truncated (503 AA)
20			Subclass: carboxylesterase 2; intestinal carboxylesterase; liver carboxylesterase-2
			Subclass: Similar to carboxylesterase 2 (intestine, liver)
25	AK014166 BAB29187.1	F:(C-D) -1.58	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1)
			Alternate: Similar to transmembrane 7 superfamily member 2
			Alternate: lamin B receptor
			Alternate: similar to Lamin B receptor (Integral nuclear envelope inner membrane protein) (LMN2R)
			Alternate: integral nuclear envelope inner membrane protein
30	AK005060 BAB23784.1	F:(C-IR)-2.5 8 F:(C-D)-2.09	alanine-glyoxylate aminotransferase
			Subclass: alanine-glyoxylate aminotransferase 2
			Subclass: alanine-glyoxylate aminotransferase 2-like 1
35	NM_015814 NP_056629. 1	F:(C-D)-2.18	Wnt signalling inhibitors

		Subclass: Dickkopf-3
		Subclass: dickkopf homolog 3; RIG-like 7-1; RIG-like 5-6
		Subclass: REIC protein
5	NM_023478 NP_075967. 1	F:(C-IR)-2.0 8 uroplakin
		Subclass: uroplakin 3
10	NM_010289 NP_034419. 1	F:(C-D)-2.07 Gap junction membrane channel protein
		Subclass: connexin
		Subclass: connexin 62
15		Subclass: connexin 58
		Subclass: connexin 59; gap junction alpha 10
		Subclass: Gap junction alpha-8 protein (Connexin 50) (Cx50)
		Subclass: Gap junction alpha-3 protein (Connexin 46) (Cx46).
		Subclass: gap junction protein, alpha 5, 40kDa (connexin 40)
20		Subclass: Gap junction alpha-4 protein (Connexin 37) (Cx37).
		Subclass: connexin 43; gap junction protein, alpha 1, 43kD
		Subclass: gap junction protein, alpha 7, 45kDa (connexin 45)
		Subclass: gap junction protein, beta 2, 26kDa (connexin 26)
		Subclass: connexin46.6
25		
	NM_008118 NP_032144. 1	F:(C-IR)-2.0 1 U:(IR-D)+2. 26 intrinsic factor
		Subclass: gastric intrinsic factor (vitamin B synthesis); Gastric intrinsic factor
30		
	NM_010275 NP_034405. 1	F:(C-D)-2.00 neurotrophic factor
		Subclass: glial cell line derived neurotrophic factor
35		Subclass: astrocyte-derived trophic factor 1, ATF-1 [human, caudate,].
	NM_010004 NP_034134. 1	F:(IR-D)-2.0 0 cytochrome P-450
40		Subclass: cytochrome P450, family 2
		Subclass: Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C).
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 19
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9;
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8)

		Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1)
		Subclass: cytochrome P450 2C17
		Subclass: cytochrome P450 2E1
5		Subclass: cytochrome P450, subfamily IIC, polypeptide 8 isoform 2
		Subclass: cytochrome P450 2F1
		Subclass: cytochrome P450 2A3, hepatic - human
		Subclass: cytochrome P450 2A4 - human
		Subclass: coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6
10		Subclass: Cytochrome P450 2A7 (CYP11A7) (P450-IIA4).
		Subclass: Cytochrome P450 2A13 (CYP11A13).
		Subclass: cytochrome P450, family 2, subfamily B, polypeptide 6
		Subclass: cytochrome P450, subfamily IIS, polypeptide 1
		Subclass: cytochrome P450 2J2
15		Subclass: cytochrome P-450 HPH (120 AA)
		Subclass: cytochrome P450 IID6
		Subclass: cytochrome P450db1
		Subclass: cytochrome P450, family 1, subfamily A, polypeptide 1
		Subclass: cytochrome P450 CYP1B1
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## SUBTABLE 2B - Unfavorable

Main	Behavior	Human Protein Name
5 NM_019634 NP_062608. 1	U:(HI-D) 2.86	transmembrane 4 superfamily
		Subclass: transmembrane 4 superfamily member 2; membrane component, x chromosome, surface marker 1; T-cell acute lymphoblastic leukemia associated antigen 1; transmembrane protein A15; tetraspanin protein; cell surface glycoprotein A15; CD231 antigen; transmembrane 4 superfamily 2b
		Subclass: transmembrane 4 superfamily member 6; tetraspan TM4SF; A15 homolog; tetraspanin TM4-D; tetraspanin 6
10 NM_016875 NP_058571. 1	U:(HI-D) 2.73	germ cell specific Y-box binding protein; contrin
15 AF001293 AAB58795. 1	U:(HI-D) 2.59	zinc finger protein,
		Subclass: similar to zinc finger protein, subfamily 1A, 3 (Aiolos)
		Subclass: zinc finger protein, subfamily 1A, 3 (Aiolos)
		Subclass: AIOLOS isoform four
20		Subclass: AIOLOS isoform two
		Subclass: AIOLOS isoform three
		Subclass: AIOLOS isoform six
		Subclass: AIOLOS isoform five
		Subclass: zinc finger protein, subfamily 1A, 1 (Ikaros); Ikaros (zinc finger protein)
25		Subclass: zinc finger protein, subfamily 1A, 2 (Helios); zinc finger DNA binding protein Helios
		Subclass: Similar to zinc finger protein, subfamily, 1A, 2 (Helios)
		Subclass: zinc finger protein, subfamily 1A, 4 (Eos); zinc finger transcription factor Eos
30 NM_009895 NP_034025. 1	U:(HI-D) 2.45	cytokine-inducible SH2-containing protein
		Subclass: cytokine-inducible SH2-containing protein isoform 2; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling
		Subclass: cytokine-inducible SH2-containing protein isoform 1; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling
35 NM_018830 NP_061300. 1	U:(HI-D) 2.42	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2; N-acylsphingosine amidohydrolase 2; mitochondrial ceramidase; N-acylsphingosine amidohydrolase (acid ceramidase) 2
NM_008597 NP_032623. 1	U:(HI-D) 2.36	matrix Gla protein
40 NM_009234 NP_033260. 1	U:(HI-D) 2.36	SRY (sex determining region Y)-box 11; SRY (sex-determining region Y)-box 11
AF398969 AAK97491. 1	U:(HI-D) 2.35	ankyrin repeat and SOCS box-containing 8



5	NM_016970 NP_058666. 1	U:(HI-D) 2.13	killer cell lectin-like receptor subfamily G, member 1; mast cell function-associated antigen (ITIM-containing)
10	NM_009344 NP_033370. 1	U:(HI-D) 2.1	pleckstrin homology-like domain, family A, member 1; PQ-rich protein
			Alternate: Similar to T-cell death associated gene
15	NM_009964 NP_034094. 1	U:(HI-D) 2.06	crystallin, alpha B; crystallin, alpha-2; Rosenthal fiber component; heat-shock 20 kD like-protein
20	NM_013565 NP_038593. 1	U:(HI-D) 2.05	integrin alpha
			Subclass: VLA-3 alpha subunit
25			Subclass: integrin alpha-3 (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c)
			Subclass: integrin alpha 3 isoform b
30			Subclass: integrin alpha 6
			Subclass: integrin alpha-6 chain precursor, splice form A
35			Subclass: integrin alpha-6 chain precursor, splice form B
			Subclass: integrin alpha 7
40	NM_013805 NP_038833. 1	U:(HI-D) 2.04	transmembrane protein claudin 5; androgen withdrawal and apoptosis induced protein RVP1 (rat)-like; Claudin-5 (transmembrane protein deleted in velocardiofacial syndrome)
45	AK014697 BAB29508. 1	U:(HI-D) 2.01	DC-specific transmembrane protein
50	NM_009255 NP_033281. 1	U:(HI-D) 2.01	similar to tropomyosin, fibroblast - human
			Alternate: Protease Inhibitor; Proteinase Inhibitor
55			Subclass: Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease Inhibitor 7)
			Subclass: Plasminogen Activator Inhibitor-1; Chain: A; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai
60			Subclass: serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1; plasminogen activator inhibitor, type I; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai
			Subclass: prebeta-migrating plasminogen activator inhibitor
65			Subclass: Cleaved Substrate Variant Of Plasminogen Activator Inhibitor-1
			Subclass: Active Form Of Human Pai-1
70			Subclass: serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1; protease Inhibitor 12 (neuroserpin)
			Subclass: serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1
75			Subclass: protease inhibitor 14; pancpn
80	NM_017480 NP_059508. 1	U:(C-HI) 6.6	inducible T-cell co-stimulator; activation-inducible lymphocyte immunomediatory molecule; inducible costimulator
			Alternate: Similar to inducible T-cell co-stimulator

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NM_011704 NP_035834. 1	U (C-HI) 4.37, U (C-D) 3.14, U (HI-D) 2.37	Vanin
		Vanin 1 (VNN1); pantetheinase
		vanin 3 isoform 1 ; VNN3 protein; pantetheinase
		vanin 2, isoform 1 ; Vannin 2; pantetheinase
		vanin 2, isoform 2; Vannin 2; pantetheinase
		Alternate: Blotidinase
M12571 AAA57234. 1	U:(C-HI) 3.58	heat shock 70kDa protein
		Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
		Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
		Subclass: heat shock 70kD protein 1-like
		Subclass: heat shock 70kDa protein 6 (HSP70B)
		Subclass: heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2
NM_007585 NP_031611. 1	U:(C-HI) 3.49, U:(C-D) 4.83	Annexin
		Subclass: annexin A2; annexin II; lipocortin II; Annexin II (lipocortin I); calpactin I, heavy polypeptide (p36); annexin II (lipocortin II; calpactin I, heavy polypeptide); annexin II (lipocortin II)
		Subclass: bA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))
		Subclass: annexin I; annexin I (lipocortin I); lipocortin I
		Subclass: Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41)
		Subclass: annexin A11; annexin XI; autoantigen, 56-kD; calcyclin-associated annexin 50
		Subclass: annexin VI isoform 2; annexin VI (p68); calcium-binding protein p68; calphobindin II;
		Subclass: annexin VI isoform 1; annexin VI (p68); calcium-binding protein p68; calphobindin II; calelectrin F498
		Subclass: Annexin III
		Subclass: annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calcimedlin 35-alpha); calcimedlin 35-alpha
		Subclass: Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutation With Glu 17 Replaced By Gly (E17G)
		Subclass: annexin A5
		Subclass: annexin VIII; Annexin VII
		Subclass: similar to annexin A8
		Subclass: annexin VII isoform 2; annexin VII (synexin); synexin
		Subclass: annexin VII isoform 1; annexin VII (synexin); synexin
		Subclass: annexin A13 isoform b
		Subclass: annexin A13; annexin XIII; annexin, intestine-specific
		Subclass: annexin 31; annexin XXXI
		Subclass: keratinocyte annexin-like protein
		Alternate: protein PP4-X
		Alternate: protein p68 (1 - 673)

	NM_007980 NP_032006. 1	U:(C-HI) 3.49, U:(C-D) 2.22	intestinal fatty acid binding protein 2; Fatty acid-binding protein, intestinal; I-FABP; fatty acid binding protein 2, intestinal
5	NM_007809 NP_031835. 1	U:(C-HI) 3.41, U:(C-D) 3.69	cytochrome P450
			Subclass: cytochrome P450, subfamily XVII polypeptide; steroid 17-alpha-monooxygenase; steroid 17-alpha-hydroxylase/17,20 lyase; cytochrome p450 XVIIA1
			Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase
10			Subclass: cytochrome P450-1A2
			Subclass: cytochrome P450 4
			Subclass: Cytochrome P450 XXIB (Steroid 21-hydroxylase) (P450-C21B)
			Subclass: cytochrome P450, subfamily XXIA polypeptide 2; steroid 21-monooxygenase; steroid 21-hydroxylase
			Subclass: cytochrome P450 CYP1B1
15	AK007868 BAB25319. 1	U:(C-HI) 3.19, U:(C-D) 2.42	chromosome 11 open reading frame 24
20	U67189 AAB50619. 1	U:(C-HI) 3.17	Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R) (A28-RGS14P)
25	M63245 AAA91867. 1	U:(C-HI) 3.05	aminolevulinate synthase
			Subclass: aminolevulinate synthase 1
			Subclass: 5-aminolevulinic acid synthase
			Subclass: 5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-E)
30			Subclass: aminolevulinate, delta-, synthase 2; Aminolevulinate, delta-, synthase-2
			Subclass: Similar to aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)
35	NM_007437 NP_031463. 1	U:(C-HI) 3.02	Aldehyde dehydrogenase
			Subclass: similar to fatty aldehyde dehydrogenase
			Subclass: aldehyde dehydrogenase 3A2; aldehyde dehydrogenase 10; aldehyde dehydrogenase 3 family, member A2; fatty aldehyde dehydrogenase
			Subclass: aldehyde dehydrogenase 3 family, member A1; aldehyde dehydrogenase, dimeric NADP-prefering; acetaldehyde dehydrogenase; ALDH, stomach type
			Subclass: aldehyde dehydrogenase 3B1; aldehyde dehydrogenase 7; aldehyde dehydrogenase 3
40			Subclass: Similar to aldehyde dehydrogenase 3 family, member B1
			Subclass: aldehyde dehydrogenase 3B2; aldehyde dehydrogenase 8; aldehyde dehydrogenase 3
			Subclass: Similar to aldehyde dehydrogenase 3 family, member B2

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NM_022331 NP_071726. 1	U:(C-HI) 3.00, U:(C-D) 2.29	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene
		Alternate: Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
NM_007468 NP_031494. 1	U (C-HI) 2.98, U (C-D) 2.42, U (HI-D) 2.16	Apolipoprotein A-IV (Apo-AIV)
NM_007837 NP_031863. 1	U:(C-HI) 2.98, U:(C-D) 2.16	DNA-damage-inducible transcript 3; C/EBP homologous protein; growth arrest- and DNA damage-inducible
		Alternate: TLS-CHOP
		Alternate: DNA-damage-inducible protein GADD153 - human
NM_007860 NP_031886. 1	U:(C-HI) 2.84, U:(C-D) 2.06	Type I iodothyronine deiodinase (Type-I 5'deiodinase) (DIO1) (Type 1 DI) (5DI)
		Alternate: Similar to deiodinase, iodothyronine, type I
NM_016974 NP_058670. 1	U (C-HI) 2.79, U (C-D) 4.24, U (HI-D) 2.47	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)
AK007378 BAB24997. 1	U:(C-HI) 2.77	hypothetical protein MGC4504
NM_011375 NP_035505. 1	U:(C-HI) 2.65, U:(C-D) 2.16	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase); ganglioside G(M3) Synthase
		Alternate: Gal beta 1,3(4) GlcNAc alpha 2,3-sialyltransferase
NM_007760 NP_031786. 1	U:(C-HI) 2.57, U:(C-D) 2.16	caritine acetyltransferase
		Subclass: Carnitine O-acetyltransferase (Carnitine acetylase) (CAT)
		Subclass: carnitine acetyltransferase isoform 1
		Subclass: carnitine acetyltransferase isoform 2
		Subclass: carnitine acetyltransferase isoform 3
NM_020570 NP_065595. 1	U:(C-HI) 2.55	X-ray repair cross complementing protein 2; X-ray repair, complementing defective, repair in Chinese hamster; DNA repair protein XRCC2

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NM_019423 NP_062296. 1	U:(C-HI) 2.53, U:(C-D) 2.08	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
		Alternate: elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4; Stargardt disease 3 (autosomal dominant)
NM_019977 NP_064361. 1	U:(C-HI) 2.51	unknown protein
		Alternate: aldehyde reductase (aldose reductase) like 6; similar to mouse aldehyde reductase 6 (renal); myo-inositol oxygenase; kidney-specific protein 32
NM_031162 NP_112439. 1	U:(C-HI) 2.49	CD32 antigen, zeta polypeptide (TIT3 complex)
NM_019699 NP_062673. 1	U:(C-HI) 2.46	fatty acid desaturase
		Subclass: fatty acid desaturase 2; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase
		Subclass: fatty acid desaturase 3; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase
		Subclass: fatty acid desaturase 1; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5 desaturase; delta-5 fatty acid desaturase
NM_023719 NP_076208. 1	U:(C-HI) 2.36, U:(C-D) 2.42	thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3
NM_013760 NP_038788. 1	U:(C-HI) 2.34, U:(C-D) 2.1	DnaJ (Hsp40) homolog, subfamily B, member 9; microvascular endothelial differentiation gene 1; DKFZP564F1862 protein; endoplasmic reticulum DnaJ homolog 4
		Alternate: similar to putative microvascular endothelial differentiation gene 1; similar to X98993 (PID:g1771560)
NM_023184 NP_075673. 1	U:(C-HI) 2.34	Kruppel-like factor 15; KKLf protein; kidney-enriched Kruppel-like factor
NM_018791 NP_061261. 1	U:(C-HI) 2.32	Zinc finger protein
		Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)
		Subclass: zinc finger protein 226; Kruppel-associated box protein
		Subclass: Zinc finger protein ZNF45
		Subclass: similar to Zinc finger protein 229
		Subclass: zinc finger protein 224
		Subclass: zinc finger protein 228
		Subclass: similar to ZNF228 protein
		Subclass: Zinc finger protein 234 (Zinc finger protein HZF4)
		Subclass: similar to Zinc finger protein 234 (Zinc finger protein HZF4)
		Subclass: zinc finger protein 225

	AK007864 BAB25316. 1	U:(C-HI) 2.31	similar to RIKEN cDNA 1810054O13
5	NM_019545 NP_062418. 1	U:(C-HI) 2.31	hydroxyacid oxidase
			Subclass: hydroxyacid oxidase 3; medium-chain 2-hydroxy acid oxidase HAOX3; (S)-2-hydroxy-acid oxidase; glycolate oxidase
			Subclass: hydroxyacid oxidase 2; long-chain L-2-hydroxy acid oxidase; (S)-2-hydroxy-acid oxidase; glycolate oxidase
10			Subclass: hydroxyacid oxidase 1; (S)-2-hydroxy-acid oxidase; glycolate oxidase
	NM_011058 NP_035188. 1	U:(C-HI) 2.3	platelet-derived growth factor receptor
15			Subclass: platelet-derived growth factor receptor alpha polypeptide
			Subclass: platelet-derived growth factor receptor beta; beta platelet-derived growth factor receptor
			Alternate: vascular endothelial growth factor receptor
			Subclass: Vascular endothelial growth factor receptor 3 (VEGFR-3) (Tyrosine-protein kinase receptor FLT4)
			Subclass: vascular endothelial growth factor receptor 2
20			Alternate: KIT protein
			Alternate: colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms)
			Alternate: Macrophage colony stimulating factor 1 receptor (CSF-1-R) (Fms proto-oncogene)
			Alternate: FLT3 receptor tyrosine kinase
			Alternate: fms-related tyrosine kinase 3
25			Alternate: fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability
			Alternate: fms-related tyrosine kinase 4; fms-related tyrosine kinase-4 (vascular endothelial growth factor receptor 3)
	NM_010565 NP_034695. 1	U:(C-HI) 2.28	inhibin beta C chain preproprotein; activin beta-C chain
30			Alternate: activin beta E
	NM_011994 NP_036124. 1	U:(C-HI) 2.27	ATP-binding cassette, sub-family D
35			Subclass: ATP-binding cassette, sub-family D, member 2; adrenoleukodystrophy-like 1; hALDR
			Subclass: ATP-binding cassette, sub-family D (ALD), member 1; adrenoleukodystrophy protein
			Subclass: ATP-binding cassette, sub-family D, member 3; Peroxisomal membrane protein-1 (70kD); peroxisomal membrane protein 1 (70kD, Zellweger syndrome); peroxisomal membrane protein-1
	NM_018817 NP_061287. 1	U:(C-HI) 2.27	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1; HepA-related protein; SMARCA-like protein 1
40			
	AK006096 BAB24407. 1	U:(C-HI) 2.24	Similar to RIKEN cDNA 1700018O18 gene
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	NM_019682 NP_062656. 1	U:(C-HI) 2.24	dynein, cytoplasmic, light polypeptide; Dynein, cytoplasmic, light chain (protein inhibitor of neuronal NOS); protein inhibitor of neuronal nitric oxide synthase
5	NM_009154 NP_033180. 1	U:(C-HI) 2.23	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, 5A
			Alternate: KIAA1445 protein
			Alternate: similar to KIAA1445 protein
10	AK005274 BAB23924. 1	U:(C-HI) 2.22, U:(C-D) 2.15	hypothetical protein MGC2605
			Alternate: similar to hydroxyacyl glutathione hydrolase 2
15	NM_009315 NP_033341. 1	U:(C-HI) 2.2	TBP-associated factor 6 Subclass:
			Subclass: TBP-associated factor 6 isoform gamma; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit
			Subclass: TBP-associated factor 6 isoform delta; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit
20	NM_011361 NP_035491. 1	U:(C-HI) 2.2	serine/threonine protein kinase sgk (serum/glucocorticoid regulated kinase).
			Alternate: serum/glucocorticoid regulated kinase-like; cytokine-independent survival kinase
			Alternate: v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B
25	NM_011844 NP_035974. 1	U:(C-HI) 2.19	monoglyceride lipase
30	NM_018861 NP_061349. 1	U:(C-HI) 2.18	solute carrier family 1 (glutamate/neutral amino acid transporter)
			Subclass: solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; Solute carrier family 1 (glutamate/neutral amino acid transporter),
			Subclass: solute carrier family 1 (neutral amino acid transporter), member 5; baboon M7 virus receptor; RD114 virus receptor; neutral amino acid transporter B
35			Alternate: sodium-dependent neutral amino acid transporter type 2 truncated isoform
			Alternate: neutral amino acid transporter B
40	AF213258 AAG43836	U:(C-HI) 2.17, U:(C-D) 2.34	membrane-associated guanylate kinase-related 3
			Alternate: similar to membrane-associated guanylate kinase MAGI3
			Alternate: MAGI-1A
			Alternate: MAGI-1C beta
			Alternate: MAGI-1B alpha beta
			Alternate: dJ730K3.2 (similar to BAI1-associated protein)
45			Alternate: atrophin-1 interacting protein 1; activin receptor interacting p; KIAA0705 gene product

		Alternate: BAI1-associated protein 1; WW domain-containing protein 3
		Alternate: brain-specific angiogenesis inhibitor-associated protein 1
5	NM_008382 NP_032408.1	U:(C-HI) 2.13 activin beta E
		Alternate: inhibin beta C chain preproprotein; activin beta-C chain
10	NM_011579 NP_035709.1	U:(C-HI) 2.13 hypothetical protein R30953_1
	NM_007679 NP_031705.1	U:(C-HI) 2.11 CCAAT/enhancer binding protein (C/EBP), delta
15		Alternate: similar to CCAAT/enhancer binding protein delta (C/EBP delta) (Nuclear factor NF-IL6-beta) (NF-IL6-beta)
	NM_030887 NP_112149.1	U:(C-HI) 2.07 Jun dimerization protein
20	NM_009366 NP_033392.1	U:(C-HI) 2.06, U:(C-D) 2.89, U:(HI-D) 2.64 transforming growth factor beta-stimulated protein TSC-22
		Alternate: cerebral protein-2
25	NM_019992 NP_064376.1	U:(C-HI) 2.06, U:(C-D) 2.23, U:(HI-D) 2.12 BCR downstream signaling 1
	NM_019415 NP_062288.1	U:(C-HI) 2.06 Solute carrier family 12
30		Subclass: Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter)
		Subclass: solute carrier family 12 (sodium/potassium/chloride transporters), member 2; Solute carrier family 12 (sodium/potassium/chloride transporters),
		Subclass: solute carrier family 12 (potassium/chloride transporters), member 7;
		Subclass: solute carrier family 12, (potassium-chloride transporter) member 5
35	AK002693 BAB22288.1	U:(C-HI) 2.04 diacylglycerol O-acyltransferase 2 like 1; diacylglycerol acyltransferase 2-like
40	AK003722 BAB22959.1	U:(C-HI) 2.04 ubiquitin-conjugating enzyme E2C; ubiquitin carrier protein E2-C
45	NM_010516 NP_034646.1	U:(C-HI) 2.04 CYR61 protein (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (IGF1 protein)
		Alternate: connective tissue growth factor



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		Alternate: WNT1 inducible signaling pathway protein 1, isoform 1 precursor; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1; wnt-1 signaling pathway protein 1; connective tissue growth factor related protein WISP-1; Wnt-1 induced secreted protein 1
		Alternate: WNT1 inducible signaling pathway protein 3, isoform 2; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3
		Alternate: WNT1 inducible signaling pathway protein 3, isoform 1; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3
	NM_010354 NP_034484. 1	U:(C-HI) 2.03 gelsolin (amyloidosis, Finnish type); Gelsolin
		Alternate: scinderin; adseverin; KIAA1905 protein
		Alternate: villin 1; Villin-1
		Alternate: similar to mouse adseverin(D5); similar to PID:g2218019
		Alternate: Advillin (p92)
		Alternate: Similar to gelsolin (amyloidosis, Finnish type)
		Alternate: Similar to advillin
	AK002717 XP_134867	U:(C-HI) 2.02 RNA, U transporter 1; snurportin-1; snuportin-1
	AK004600 BAB23401. 1	U:(C-HI) 2.02 Rho guanine nucleotide exchange factor 3; RhoGEF protein; 59.8 kDa protein
		Alternate: Similar to Rho guanine nucleotide exchange factor (GEF) 3
	M62766 AAA37819. 1	U:(C-HI) 2.02 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
		Subclass: Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
	NM_008299 NP_032325. 1	U:(C-HI) 2.02 DnaJ (Hsp40) homolog
		Subclass: DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
		Subclass: similar to DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
		Subclass: similar to DnaJ homolog subfamily B member 8 (mDJ6)
	NM_010877 NP_035007. 1	U:(C-HI) 2.02 Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH oxidase factor 2) (67 kDa neutrophil oxidase factor) (p67-phox)
		Alternate: Similar to neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)
		Alternate: p67phox-like protein
	NM_019643 NP_062617. 1	U:(C-HI) 2.02 TERA protein
	NM_013594 NP_038622. 1	U:(C-HI) 2.01, U:(C-D) 2.15 methyl-CpG binding protein 1
		Subclass: methyl-CpG binding domain protein 1 isoform 1
		Subclass: methyl-CpG binding protein splice variant 1
		Subclass: methyl-CpG binding domain protein 1 isoform 2

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		Subclass: methyl-CpG binding protein splice variant 2
		Subclass: methyl-CpG binding domain protein 1 isoform PCM1
		Subclass: methyl-CpG binding domain protein 1 isoform 3
		Subclass: methyl-CpG binding domain protein 1 isoform 4
5		
	NM_025566 NP_079842. 1	U:(C-HI) 2 hypothetical protein MGC17791
		Alternate: similar to RIKEN cDNA 2600017J23
10		
	AK004002 BAB23117. 1	U:(C-HI) 2 five-lipoxygenase activating protein (FLAP)
15		
	NM_021366 NP_067341. 1	U:(C-HI) 2 Kruppel-like factor 13; transcription factor NSLP1; novel Sp1 like zinc finger transcription factor; RANTES factor of late activated T lymphocytes-1; basic transcription element binding protein 3
		Alternate: similar to Krueppel-like factor 13 (Transcription factor BTEB3) (Basic transcription element binding protein 3) (BTE-binding protein 3) (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Transcription factor NSLP1) (Novel Sp1-like zinc fi
20		
	NM_010721 NP_034851. 1	U:(C-D) 7.08 lamin
		Subclass: lamin B1
		Subclass: Similar to lamin B1
25		Subclass: Lamin B2
		Subclass: lamin A/C isoform 2; 70 kDa lamin
		Subclass: Similar to lamin A/C
		Alternate: lamin A protein
30		
	NM_026228 NP_080504. 1	U:(C-D) 4.88 protein up-regulated by BCG-CWS
		Alternate: unnamed protein product
		Alternate: KIAA0062
35		Alternate: similar to KIAA0062
		Alternate: Unknown (protein for MGC:23235)
40		
	NM_026156 NP_080432. 1	U:(C-D) 3.75 similar to PP3898
		Alternate: XAB2
		Alternate: KIAA1177 protein
		Alternate: HCNP protein; XPA-binding protein 2
		Alternate: Similar to HCNP protein; XPA-binding protein 2
		Alternate: FLJ00081 protein
45		
	U70139 AAB62717. 1	U:(C-D) 3.08, U:(HI-D) 2.08 nocturnin
		Alternate: CCR4 carbon catabolite repression 4-like (S. cerevisiae); CCR4-like (carbon catabolite repression 4, S. cerevisiae)
50		
	NM_008137 NP_032163. 1	U:(C-D) 3.01 guanine nucleotide binding protein (G protein)

		Subclass: guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14
		Subclass: GTP-binding protein alpha q
		Subclass: Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)
5		Subclass: guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
		Subclass: similar to GNA15; ALPHA-16
		Subclass: similar to Guanine nucleotide-binding protein, alpha-11 subunit (GL2)
		Subclass: Guanine nucleotide-binding protein G(O), alpha subunit 2
		Subclass: guanine nucleotide binding protein alpha oB
		Subclass: Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein)
10		Subclass: Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
		Subclass: guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3; 87U6
		Subclass: similar to Guanine nucleotide-binding protein G(T), alpha-3 subunit (Gustducin alpha-3 chain)
15	C76314 NP_690023. 1	U:(C-D) 2.97 KIAA0432
		Alternate: CDC5-like; CDC5 (cell division cycle 5, S. pombe, homolog)-like; Cell division cycle 5, S. pombe, homolog-like; Cdc5-related protein
20	AK009292 BAB26196. 1	U:(C-D) 2.94, U:(HI-D) 2.87
		solute carrier family 27 (fatty acid transporter)
		Subclass: solute carrier family 27 (fatty acid transporter), member 4; fatty acid transport protein 4
		Subclass: solute carrier family 27 (fatty acid transporter), member 5; very long-chain acyl-CoA synthetase homolog 2; very long-chain acyl-CoA synthetase-related protein; likely ortholog of mouse solute carrier family 27 (fatty acid transporter), member 5
25		Subclass: solute carrier family 27 member 3; fatty acid transport protein 3
		Subclass: solute carrier family 27 (fatty acid transporter), member 2; very long-chain fatty-acid-coenzyme A ligase 1; very-long-chain acyl-CoA synthetase
		Alternate: Unknown (protein for MGC:16752)
		Alternate: very long-chain acyl-CoA synthetase homolog 1
		Alternate: Unknown (protein for IMAGE:3613739)
		Alternate: Similar to hypothetical protein MGC4365
30	M12573 AAA37863. 1	U:(C-D) 2.94 heat shock 70kDa protein
		Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
35		Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
		Subclass: heat shock 70kD protein 1-like
		Subclass: heat shock 70kDa protein 6 (HSP70B*)
		Subclass: heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2
40	AK017185 BAB30625. 1	U:(C-D) 2.9 Ras-related protein Rab-30
45	AK018132 BAB31086. 1	U:(C-D) 2.44 KIAA1001 protein
		Alternate: Similar to KIAA1001 protein

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		Alternate: Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8
		Alternate: Similar to arylsulfatase A
		Alternate: N-acetylgalactosamine-6-sulfatase precursor; Galactosamine (N-acetyl)-6-sulfate sulfatase; chondroitinase
		Alternate: Unknown (protein for MGC:24090)
		Alternate: arylsulfatase F
		Alternate: similar to arylsulfatase F
		Alternate: Unknown (protein for MGC:31932)
		Alternate: arylsulfatase D precursor, isoform a
	AK004984 BAB23719. 1	U:(C-D) 2.38 cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
	NM_011128 NP_035258. 1	U:(C-D) 2.35, U:(HI-D) 2.73 lipase
		Subclass: pancreatic lipase
		Subclass: pancreatic lipase-related protein 2
		Subclass: pancreatic lipase-related protein 1
	NM_008239 NP_032265. 2	U:(C-D) 2.23, U:(HI-D) 2.15 winged helix/forkhead transcription factor
		Alternate: HNF-3/forkhead-like protein 1
	AK013002 BAB28588. 1	U:(C-D) 2.21 general transcription factor IIF, polypeptide 1 (74kD subunit)
		Alternate: RAP74
		Alternate: Transcription Initiation Factor Iif, Subunit; Chain: A, C, E, G; Fragment: Residues 2-119; Synonym: Transcription Initiation Factor Rap30
	AK007293 BAB24937. 1	U:(C-D) 2.19, U:(HI-D) 2.62 KIAA1879 protein
	NM_019521 NP_062394. 1	U:(C-D) 2.14 growth arrest-specific 6; AXL stimulatory factor
		Alternate: protein S (alpha); Protein S, alpha
		Alternate: Vitamin K-dependent protein S precursor
	NM_011693 NP_035823. 1	U:(C-D) 2.08 vascular cell adhesion molecule
		Subclass: vascular cell adhesion molecule 1, isoform a ; CD106 antigen
		Subclass: vascular cell adhesion molecule 1, isoform b precursor; CD106 antigen
		Subclass: Vascular Cell Adhesion Protein 1; Chain: A; Fragment: Vcam-D1, D2 (Integrin Binding Fragment); Synonym: Vcam-1
		Subclass: Vascular Cell Adhesion Molecule-1; Chain: A, B; Fragment: N-Terminal Two-Domain Fragment; Synonym: Vcam-1; Engineered: Yes; Mutation: Y196D; Other_Details: Hybrid Molecule Composed Of Vcam-1 Domains 1 and 2 Fused To IgG, Hinge and Fc

	U70210 AAC53593. 1	U:(C-D) 2.06	Amyloid beta A4 precursor protein-binding family B (Fe65-like protein)
5			Subclass: Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)
			Subclass: similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)
			Subclass: amyloid beta A4 precursor protein-binding, family B, member 1 isoform delta E9; amyloid beta A4 precursor protein-binding, family B, member 1; stat-like protein; adaptor protein FE65a2
			Subclass: adaptor protein FE65a2
			Subclass: FE65-like protein 2 isoform a; amyloid precursor interacting protein
10			Subclass: Similar to FE65-LIKE 2
			Subclass: FE65-like protein 2 isoform b; amyloid precursor interacting protein
			Subclass: FE65-like protein 2 isoform c; amyloid precursor interacting protein
15	NM_020277 NP_064673. 1	U:(C-D) 2.05, U:(HI-D) 2.32	transient receptor potential cation channel
			Subclass: transient receptor potential cation channel, subfamily M, member 5; MLSN1 and TRP-related; MLSN1- and TRP-related; LTRPC5 protein
			Subclass: transient receptor potential cation channel, subfamily M, member 4
			Subclass: transient receptor potential-related channel 7, a novel putative Ca2+ channel protein
20			Subclass: transient receptor potential cation channel, subfamily M, member 2; transient receptor potential-related channel 7, a novel putative Ca2+ channel protein; transient receptor potential channel 7
			Subclass: transient receptor potential cation channel, subfamily M, member 8
			Subclass: transient receptor potential cation channel, subfamily M, member 6
			Subclass: transient receptor potential cation channel, subfamily M, member 1; melastatin 1 [
			Subclass: TRP-related cation influx channel
25			Subclass: channel-kinase 1
			Subclass: similar to LTRPC7
			Alternate: melastatin 1
30	NM_019922 NP_064306. 1	U:(C-D) 2.05	cartilage associated protein
	NM_011676 NP_035806. 1	U:(C-D) 2.04	unc119 (C.elegans) homolog, isoform a; unc119 (C.elegans) homolog; retinal protein 4
35			Alternate: unc119 (C.elegans) homolog, isoform b; unc119 (C.elegans) homolog; retinal protein 4
	AF241249 AAG02285. 1	U:(C-D) 2.03	Unknown (protein for MGC:16590)
40			Alternate: Unknown (protein for IMAGE:3029289)
			Alternate: FLJ00103 protein
			Alternate: similar to FLJ00103 protein
			Alternate: Unknown (protein for MGC:20519)
			Alternate: KIAA1863 protein
			Alternate: unnamed protein product
45	NM_010220 NP_034350. 1	U:(C-D) 2.02	FK506-binding protein

		Subclass: FK506-binding protein 5; 51 kDa FK506-binding protein 5; 54 kDa progesterone receptor-associated immunophilin; T-cell FK506-binding protein; peptidylprolyl cis-trans isomerase; rotamase; FF1 antigen; HSP90-binding immunophilin
		Subclass: FK506-binding protein 4; FK506-binding protein 4 (59kD); T-cell FK506-binding protein, 59kD; p59 protein; HSP binding immunophilin; peptidylprolyl cis-trans isomerase; rotamase; FK506 binding protein 4 (59kD)
		Subclass: similar to FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)
5	NM_016696 NP_057905. 1	U:(C-D) 2.02 glypican
		Subclass: glypican 1
10		Subclass: glypican 6
		Subclass: glypican 4
		Subclass: similar to Glypican-2 (Cerebroglycan) (HSPG M13)
15	NM_013692 NP_038720. 1	U:(C-D) 2.01 TGFB inducible early growth response
		Alternate: EGR alpha transcription factor - human
		Alternate: TGFB inducible early growth response 2
20	AK004865 BAB23626. 1	U:(C-D) 2 HMG CoA synthase (3-hydroxy-3-methylglutaryl-Coenzyme A synthase)
		Subclass: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
		Subclass: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
		Subclass: hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform
25		Subclass: similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)
30	NM_019810 NP_062784. 1	U:(C-D) 2 Sodium/glucose cotransporter
		Subclass: solute carrier family 5 (sodium/glucose cotransporter), member 1; Human Na <sup>+</sup> /glucose cotransporter 1 mRNA, complete cds; solute carrier family 5 (sodium/glucose transporter), member 1
		Subclass: solute carrier family 5 (low affinity glucose cotransporter), member 4; solute carrier family 5 (neutral amino acid transporters, system A), member 4; low affinity sodium glucose cotransporter
		Subclass: solute carrier family 5 (sodium/glucose cotransporter), member 2; solute carrier family 5 (sodium/glucose transporter), member 2
		Subclass: solute carrier family 5 (inositol transporters), member 3; solute carrier family 5 (inositol transporter), member 3; human solute carrier family 5, member 3, Sodium/myo-inositol cotransporter; sodium/myo-inositol cotransporter 1
		Subclass: dJ1024N4.1 (novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1))
35		Subclass: sodium/myo-inositol cotransporter 2; putative sodium-coupled cotransporter RKST1; homolog of rabbit KST1
		Subclass: putative sodium-coupled cotransporter RKST1
		Subclass: similar to 597 aa protein related to Na/glucose cotransporters
		Subclass: Sodium/myo-inositol cotransporter (Na <sup>+</sup> )/myo-inositol cotransporter)
		Alternate: hypothetical protein FLJ25217

5	NM_028780 NP_083056. 1	U:(C-D) 2	transmembrane 9 superfamily
			Subclass: transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1
			Subclass: transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2
			Subclass: similar to Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-Iso)
			Subclass: transmembrane protein TM9SF3
10			Alternate: SM-11044 binding protein
			Alternate: KIAA0255 gene product
			Alternate: endomembrane protein emp70 precursor isolog
			Alternate: unnamed protein product
			Alternate: unnamed protein product
15	NM_009252 NP_033278. 1	U:(C-D) 1.77	proteinase inhibitor
			Subclass: alpha1-antichymotrypsin
20			Subclass: similar to Alpha-1-antichymotrypsin precursor (ACT)
			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
			Subclass: chymotrypsin inhibitor
			Subclass: Cleaved Antichymotrypsin A347R
			Subclass: Cleaved Antichymotrypsin A349R
25			Subclass: Cleaved Antichymotrypsin T345R
			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4; protease inhibitor 4 (kallistatin)
			Subclass: Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4)
			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)
			Subclass: protein C inhibitor
30			Subclass: plasma serine protease inhibitor precursor
			Subclass: Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase,
			Subclass: acrosomal serine protease inhibitor
			Alternate: hypothetical protein DKFZp434P131.1
35	NM_01385 0 NP_03887 8.1	U:(C-IR)+2. 4	ATP-binding cassette transporter
			Subclass: ATP-binding cassette, sub-family A, member 7, isoform a
			Subclass: ATP-binding cassette, sub-family A, member 7, isoform b
40			Subclass: ATP-binding cassette, sub-family A member 1
			Subclass: ATP-binding cassette, sub-family A member 4
			Subclass: ATP-binding cassette, sub-family A, member 12 isoform a
			Subclass: ATP-binding cassette, sub-family A, member 12 isoform b
45			Subclass: ATP binding cassette transporter A13
			Subclass: ATP-binding cassette, sub-family A, member 2
			Subclass: ATP-binding cassette, sub-family A, member 5
			Subclass: ATP-binding cassette, sub-family A, member 9 isoform a
			Subclass: ATP-binding cassette, sub-family A, member 9 isoform b

		Subclass: ATP-binding cassette, sub-family A, member 10
		Subclass: ATP-binding cassette A6
		Subclass: ATP-binding cassette, sub-family A member 8
		Subclass: Retinal-specific ATP-binding cassette transporter (RIM transporter)



SUBTABLE 2C - Mixed (Favorable and Unfavorable)

Mouse Gene Protein	Behavior	Human Protein Name
5 AK007530 BAB25091.1	F:(C-HI) -7.8, F:(C-D) -2.61, U:(HI-D) 2.99	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
		Alternative: putative N-acetyltransferase Camello 2
		Alternative: GLA
10		Alternative: kidney- and liver-specific gene
		Alternative: hypothetical protein TSC501 [imported]
NM_007825 NP_031851.1	F:(C-HI) -6.41 U:(HI-D) 5.83	cytochrome P450, subfamily VII B, polypeptide 1; oxysterol 7alpha-hydroxylase
15 NM_015763 NP_056578.1	F:(C-HI) -3.7, U:(C-D) 3.14	Lipin
		Subclass: lipin 1
		Subclass: Similar to lipin 1
		Subclass: similar to Hypothetical protein KIAA0188
		Subclass: lipin 2
20 X71479 CAA50585.1	F:(C-HI) -3.57 F:(C-D) -2.54, U:(HI-D) 2.82	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase
25 NM_007643 NP_031669.1	F:(C-HI) -3.03 U:(C-D) 2.05, U:(HI-D) 3.33	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I)
AK007264 BAB24924.1	F:(C-HI) -2.95 U:(HI-D) 2.34	similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)
		Alternate: Uridine phosphorylase
30 NM_010379 NP_034509.1	F:(C-HI) -2.87 U:(HI-D) 2.37	MHC class II histocompatibility antigen
		Subclass: MHC class II histocompatibility antigen DQw1-beta chain precursor
		Subclass: MHC class II HLA-DQ-beta-1
		Subclass: HLA class II histocompatibility antigen, DQ(W3) beta chain precursor
35		Subclass: MHC class II histocompatibility antigen HLA-DQ beta chain (DQ4) precursor - human

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NM_020564 NP_065589.1	F:(C-HI) -2.84, F:(C-D) -2.36, U:(HI-D) 2.6	sulfotransferase family, cytosolic, 2B, member 1; sulfotransferase family 2B, member 1
		Subclass: hydroxysteroid sulfotransferase SULT2B1a
		Subclass: hydroxysteroid sulfotransferase SULT2B1b
NM_032400 NP_115776.1	F:(C-HI) -2.79, U:(HI-D) 3.03	G protein-coupled receptor 91
		Alternate: P2Y purinoceptor 1
NM_008495 NP_032521.1	F:(C-HI) -2.65, U:(C-D) 2.32	beta-galactosidase binding lectin precursor; Lectin, galactose-binding, soluble, 1; galectin
AK003129 BAB22589.1	F:(C-HI) -2.51, F:(C-D) -3.41, U:(HI-D) 3.46	Unknown (protein for IMAGE:2819455)
		Alternate: translocase of inner mitochondrial membrane 17 homolog A (yeast); preprotein translocase
NM_011596 NP_035726.1	F:(C-HI) -2.51, F:(C-D) -2.34, U:(HI-D) 4.16	TJ6 protein
		Alternate: ATPase, H <sup>+</sup> transporter
		Subclass: ATPase, H <sup>+</sup> transporting, lysosomal, non-catalytic accessory protein 1A, 110/116 kDa subunit; ATPase, H <sup>+</sup> transporting, lysosomal non-catalytic accessory protein 1 (110/116kD); vacuolar proton pump, subunit 1; clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit; vacuolar proton translocating ATPase 116 kDa subunit A isoform 1; vacuolar adenosine triphosphatase subunit Ac116; H(+)-transporting two-sector ATPase, 116 kDa accessory protein A1; vacuolar-type H(+)-ATPase 115 kDa subunit
		Subclass: ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 4; vacuolar proton pump 116 kDa accessory subunit; vacuolar proton pump, subunit 2; H(+)-transporting two-sector ATPase, noncatalytic accessory protein 1B; ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B; renal tubular acidosis; ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 2 (38kD)

		Subclass: T-cell, immune regulator 1, isoform a; ATPase, H <sup>+</sup> transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response. cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis
5	AF193796 AAL09298.1	F:(C-HI) -2.33, U:(HI-D) 3.03
		Homeobox protein Hox-C13 (Hox-3G)
		Alternate: similar to homeo box protein C13; Hox-C13 (Hox-3G)
		Alternate: unnamed protein product
10	NM_016704 NP_057913.1	F:(C-HI) -2.26, U:(HI-D) 3.29
		complement component
		Subclass: complement component C6
		Subclass: similar to Complement component C6 precursor
		Subclass: complement C7
15	NM_007870 NP_031896.1	F:(C-HI) -2.2, U:(HI-D) 2.24
		deoxyribonuclease I
		Subclass: deoxyribonuclease I-like 3
		Subclass: DNase gamma
		Subclass: deoxyribonuclease I
		Subclass: deoxyribonuclease I-like 2
20		Subclass: deoxyribonuclease I-like 1
		Subclass: DNL1L gene product
25	NM_010187 NP_034317.1	F:(C-HI) -2.18, U:(HI-D) 2.55
		Low affinity immunoglobulin gamma FC region receptor II-B precursor (FC-gamma RII-B) (FCRII-B) (IGG FC receptor II-B) (FC-gamma-RIIB) (CD32) (CDW32)
30	NM_007472 NP_031498.1	F:(C-HI) -2.17, U:(HI-D) 2.38
		aquaporin (water channel protein)
		Subclass: aquaporin 1 (channel-forming integral protein, 28kD)
		Subclass: major intrinsic protein of lens fiber; aquaporin
		Subclass: aquaporin 2; Aquaporin-2 (collecting duct)
		Subclass: hAQP-CD=collecting duct aquaporin [human, kidney, Peptide, 271 aa]
		Subclass: aquaporin 4 C2 isoform; mercurial-insensitive water channel
		Subclass: aquaporin 4 isoform a; mercurial-insensitive water channel
		Subclass: aquaporin 4, long splice form - human
		Subclass: aquaporin 5; Aquaporin-5

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NM_010024 NP_034154.1	F:(C-HI) -2.14, F:(C-D) -2.01, U:(HI-D) 2.28	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2); Dopachrome tautomerase (dopachrome delta-isomerase; tyrosinase-related protein 2)
		Alternate: tyrosinase-related protein 1
		Alternate: tyrosinase (oculocutaneous albinism IA); Tyrosinase
AF385682 AAK62363.1	F:(C-HI) -2.04, U:(HI-D) 2.02	EGF-TM7-latrophilin-related protein
		Alternate: egf-like module containing, mucin-like, hormone receptor-like sequence
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 1; egf-like module containing, mucin-like, hormone receptor-like
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module containing, mucin-like, hormone
		Subclass: egf-like module-containing mucin-like receptor 3 isoform a
		Subclass: EGF-like module EMR2
		Alternate: lectomedin
		Subclass: lectomedin-3
		Subclass: latrophilin 1; KIAA0786 protein; lectomedin-1; latrophilin
		Subclass: lectomedin-1 alpha
		lectomedin-2
		Subclass: lectomedin-2; KIAA0821 protein
		Alternate: CD97 antigen, isoform 1 precursor; leukocyte antigen CD97; seven-span transmembrane protein
		Alternate: CD97 antigen, isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein
NM_010016 NP_034146.1	F:(C-HI) -2.04, U:(HI-D) 2.14	decay-acceleration factor

		Subclass: decay accelerating factor for complement (CD55, Cromer blood group system); Decay-accelerating factor of complement
		Subclass: decay-accelerating factor, splice form 1
		Subclass: decay-accelerating factor 1 ab
		Subclass: decay-accelerating factor 4ab
5		Subclass: decay-accelerating factor 3
	NM_023740 NP_076229.1	F:(C-HI) -1.7, F:(C-D) -2.35, U:(HI-D) 2.52
		PP3774
10		Alternate: Similar to RIKEN cDNA 1500015N03 gene
		Alternate: similar to Abl-philin 2
		Alternate: hypothetical protein MGC2993
	NM_009744 NP_033874.1	F:(C-D) -4.15, U:(HI-D) 2.11
		B-cell lymphoma 6 (BCL6) protein; B-cell CLL/lymphoma-6; cys-his2 zinc finger transcription factor BCL5; zinc finger protein 51; lymphoma-associated zinc finger gene on chromosome 3
15		Alternate: similar to Bcl6-associated zinc finger protein
	NM_008245 NP_032271.1	F:(C-D) -2.62, U:(HI-D) 2.05
		hematopoietically expressed homeobox; proline-rich homeodomain-containing transcription factor (HEX)
		Alternate: Similar to hematopoietically expressed homeobox
20		
	NM_020013 NP_064397.1	U:(C-HI) 6.00, U:(C-D) 5.03, F:(HI-D) -3.06
		fibroblast growth factor 21
25	X82786 CAA58026.1	U:(C-HI) 4.07, F:(HI-D) -4.25
		antigen identified by monoclonal antibody Ki-67; Proliferation-related Ki-67 antigen
	NM_010000 NP_034130.1	U:(C-HI) 34.21, U:(C-D) 8.32, F:(HI-D) -3.81
		cytochrome P450
30		Subclass: cytochrome P450-2B6
		Subclass: Cytochrome P450 2A13 (CYP11A13)
		Subclass: cytochrome P450 2A6
		Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
		Subclass: cytochrome P450 2A4
		Subclass: Cytochrome P450 2A7 (CYP11A7) (P450-IIA4)
35		Subclass: cytochrome P450 2C8
		Subclass: cytochrome P450 2F1
		Subclass: cytochrome P450 2C18
		Subclass: cytochrome P450 2C9
		Subclass: cytochrome P450 2C10
		Subclass: cytochrome P450 2C19

		Subclass: cytochrome P450, subfamily IIA
5	NM_009689 NP_033819.1	U:(C-HI) 3.67, F:(HI-D) -3.5 baculoviral IAP repeat-containing protein 5; apoptosis inhibitor 4; survivin
		Alternate: survivin-beta
	NM_010634 NP_034764.1	U:(C-HI) 3.17, F:(HI-D) -5.62 fatty acid binding protein 5 (psoriasis-associated); E-FABP
10	NM_007659 NP_031685.1	U:(C-HI) 3.00, F:(HI-D) -2.87 Protein Kinase
		Subclass: cell division cycle 2 protein, isoform 1; cell division control protein 2 homolog; cyclin-dependent kinase 1; p34 protein kinase; cell cycle controller CDC2
		Subclass: cyclin-dependent kinase 3
		Subclass: Pcdk2/Cyclin A In Complex With Mgadp, Nitrate and Peptide Substrate
15		Subclass: Cyclin-Dependent Kinase-2; Chain: A, C; Synonym: Cdk2; Ec: 2.7.1.-
		Subclass: Cell Division Protein Kinase 2; Chain: A; Synonym: Cyclin Dependent Kinase 2; Ec: 2.7.1.37
		Subclass: PCTAIRE protein kinase 2; serine/threonine-protein kinase PCTAIRE-2; protein kinase cdc2-related PCTAIRE-2
		Subclass: Cdk5-P25(Nck5A) Complex - Protein Kinase II Catalytic Subunit, Cdk5 - Cdk5 Activator 1, Cyclin-Dependent Kinase 5 Regulatory Subunit 1, Protein Kinase II 23 Kda Subunit, Tpkii Regulatory Subunit, P23, P25, P35
20	NM_007822 NP_031848.1	U:(C-HI) 24.5, F:(C-D) -5.06, F:(HI-D) -7.06 cytochrome P450,
		Subclass: cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase (CYP4A11)
		Subclass: cytochrome P450, subfamily IVB, polypeptide 1; cytochrome P450, subfamily IVB, member 1; microsomal monooxygenase
		Subclass: cytochrome P450, subfamily IVF, polypeptide 2; leukotriene B4 omega-hydroxylase; leukotriene-B4 20-monooxygenase
25		Subclass: cytochrome P450, subfamily IVF, polypeptide 3; leukotriene B4 omega hydroxylase; leukotriene-B4 20-monooxygenase; cytochrome P450-LTB-omega
		Subclass: cytochrome P450, subfamily IVF, polypeptide 11
		Subclass: Cytochrome P450 4F12 (CYP11F12)

		Subclass: cytochrome P450, subfamily IVF, polypeptide 8; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: similar to CYTOCHROME P450 4F6 (CYP4F6)
		Subclass: cytochrome P-450LTBV
5	NM_010286 NP_034416.1	U:(C-HI) 2.83, F:(HI-D) -2.17 Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R) Alternate: hypothetical protein DKFZp566A093.1
10	NM_008362 NP_032388.1	U:(C-HI) 2.59, F:(HI-D) -2.22 interleukin 1 receptor Subclass: interleukin 1 receptor, type I Subclass: interleukin 1 receptor-like 2 Subclass: interleukin 1 receptor accessory protein-like 2
15	NM_010544 NP_034674.1	U:(C-HI) 2.45, F:(HI-D) -2.47 Indian hedgehog protein (IHH) (HHG-2) Alternate: similar to Indian hedgehog protein precursor (IHH) (HHG-2)
20	NM_011819 NP_035949.1	U:(C-HI) 2.39, U:(C-D) 2.00, F:(HI-D) -2.52 Growth/differentiation factor 15 (GDF-15); (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1) Alternate: similar to Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)...
25	NM_019641 NP_062615.1	U:(C-HI) 2.29, F:(HI-D) -2.08 stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; stathmin; leukemia-associated phosphoprotein p18 Alternate: Similar to stathmin 1/oncoprotein 18
	NM_010121 NP_034251.1	U:(C-HI) 2.15, F:(HI-D) -2.19 Eukaryotic translation initiation factor 2-alpha kinase 3 (PRKR-like endoplasmic reticulum kinase) (Pancreatic eIF2-alpha kinase) (HsPEK)
30	NM_011318 NP_035448.1	U:(C-HI) 2.03, F:(HI-D) -2.37 Serum Amyloid P Component (Sap) Alternate: C-reactive protein, pentraxin-related; C-reactive protein
35	NM_016847 NP_058543.1	U:(C-HI) 2.02, F:(HI-D) -2.03 arginine vasopressin receptor Subclass: arginine vasopressin receptor 1A; V1a vasopressin receptor; vascular/hepatic-type arginine vasopressin receptor; antidiuretic hormone receptor 1A

242

		Subclass: arginine vasopressin receptor 1B; arginine vasopressin receptor 3; antidiuretic hormone receptor 1B; vasopressin V1B receptor; pituitary vasopressin receptor 3
		Subclass: arginine vasopressin receptor 2
		Alternate: oxytocin receptor
		Alternate: vasopressin receptor type 2



	Mouse Gene Protein	Behavior	Human Protein Class
	AF001293 AAB58795.1	U (HI-D) 2.59	zinc finger protein, subfamily 1A; (Aiolos)
5	AF047725 AAD13720.1	F (HI-D) -2.06	cytochrome P450, subfamily IIC
	AF071068 AAC25566.1	F (C-HI) -2.04	dopa decarboxylase (aromatic L-amino acid decarboxylase); aromatic L-amino acid decarboxylase
		F (C-D) -2.29	
10	AF127033 AAG02285.1	F (HI-D) -2.1	fatty acid synthase; FAS
	AF193796 AAL09298.1	F (C-HI) -2.33	Homeobox protein Hox-C13
		U (HI-D) 3.03	
15	AF213258 AAG43836	U (C-HI) 2.17	membrane-associated guanylate kinase-related 3
		U (C-D) 2.34	
	AF213393 AAF31432.1	F (HI-D) -2.02	ATP-binding cassette, sub-family A
20	AF241249 AAG02285.1	U (C-D) 2.03	Unknown (protein for MGC:16590)
			Alternate: Unknown (protein for IMAGE:3029289)
			Alternate: FLJ00103 protein
25	AF294617 AAG02118.1	F (C-HI) -2.63	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase
	AF385682 AAK62363.1	F (C-HI) -2.04	EGF-TM7-latrophilin-related protein
		U (HI-D) 2.02	
30	AF398969 AAK97491.1	U (HI-D) 2.35	ankyrin repeat and SOCS box-containing 8
	AK002480 NP_666065.1	F (C-HI) -2.55	cystathionase isoform 1; cystathionine gamma-lyase; homoserine deaminase; homoserine dehydratase; cysteine desulfhydrase
		F (C-D) -2.57	
35	AK002693 BAB22288.1	U (C-HI) 2.04	diacylglycerol O-acyltransferase 2 like 1; diacylglycerol acyltransferase 2-like
	AK002717 XP_134867	U (C-HI) 2.02	RNA, U transporter 1; snurportin-1; snuportin-1
	AK002979 BAB22492.1	F (C-HI) -2.14	calcyon
40		F (C-D) -2.15	
	AK003129 BAB22589.1	F (C-HI) -2.51	Unknown (protein for IMAGE:2819455)
		F (C-D) -3.41	
		U (HI-D) 3.46	
45	AK003722 BAB22959.1	U (C-HI) 2.04	ubiquitin-conjugating enzyme E2C; ubiquitin carrier protein E2-C
	AK003797 BAB23001.1	F (C-D) -1.71	molybdenum cofactor sulfurase
			Alternate: Similar to molybdenum cofactor sulfurase

5	AK004002 BAB23117.1	U (C-HI) 2	five-lipoxygenase activating protein (FLAP)
	AK004138 BAB23187.1	F (C-D) -2.06	ORFII
			Alternative: hypothetical protein FLJ20048
10			Alternative: putative p150
	AK004600 BAB23401.1	U (C-HI) 2.02	Rho guanine nucleotide exchange factor 3; RhoGEF protein; 59.8 kDA protein
	AK004865 BAB23626.1	U (C-D) 2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
15	AK004924 BAB23675.1	F (C-D) -2.42	similar to coenzyme A diphosphatase
	AK004984 BAB23719.1	U (C-D) 2.38	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
	AK005274 BAB23924.1	U (C-HI) 2.22	hypothetical protein MGC2605
20		U (C-D) 2.15	Alternative: similar to hydroxyacyl glutathione hydrolase 2
	AK005535 BAB24106.1	F (C-HI) -2.06	solute carrier family 39 (zinc transporter), member 4
		F (C-D) -2.16	
25	AK006096 BAB24407.1	U (C-HI) 2.24	Similar to RIKEN cDNA 1700018O18 gene; unnamed protein product
	AK006128 BAB24422.1	F (C-HI) -2.71	ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter
	AK006487 BAB24612.1	F (C-HI) -2.1	hypothetical protein BC015148
30	AK006569 BAB24656.1	F (C-D) -2.18	hypothetical protein FLJ20456
			Alternative: Unknown (protein for MGC:21737)
	AK007264 BAB24924.1	F (C-HI) -2.95	similar to Uridine phosphorylase (UDRPase)
35		U (HI-D) 2.34	
	AK007293 BAB24937.1	U (C-D) 2.19	KIAA1879 protein
		U (HI-D) 2.62	
40	AK007378 BAB24997.1	U (C-HI) 2.77	hypothetical protein MGC4504
	AK007530 BAB25091.1	F (C-HI) -7.8	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
		F (C-D) -2.61	
45		U (HI-D) 2.99	
	AK007864 BAB25316.1	U (C-HI) 2.31	similar to RIKEN cDNA 1810054O13
	AK007868 BAB25319.1	U (C-HI) 3.19	chromosome 11 open reading frame 24
		U (C-D) 2.42	

5	AK007964 BAB25375.1	F (C-HI) -2.03	cholinephosphotransferase 1
		F (C-D) -2.36	
10	AK009292 BAB26196.1	U (C-D) 2.94	solute carrier family 27 (fatty acid transporter), member 4; fatty acid transport protein 4
		U (HI-D) 2.87	
15	AK009563 BAB26361.1	F (C-HI) -2.33	KIAA1434 protein
20	AK010786 BAB27182.1	F (C-D) -2.27	tubulin, beta polypeptide
			Subclass: tubulin, beta, 2
			Subclass: tubulin, beta, 4 (tubulin beta-III)
25			Subclass: tubulin, beta, 5
			Subclass: tubulin beta-1
			Alternative: similar to neu differentiation factor - human (fragment)
30	AK011896 BAB27902.1	F (C-D) -2.1	unnamed protein product
35	AK012213 BAB28101.1	F (C-HI) -2.39	aldehyde dehydrogenase 1 family
		F (C-D) -2.05	Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5
			Subclass: Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class
40			Subclass: Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)
			Subclass: Aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
			Subclass: Aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6
45	AK013002 BAB28588.1	U (C-D) 2.21	general transcription factor IIF, polypeptide 1 (74kD subunit)
			Alternate: RAP74
			Alternate: Transcription Initiation Factor Iif, Subunit; Chain: A, C, E, G; Fragment: Residues 2-119; Synonym: Transcription Initiation Factor Rap30
50	AK014166 BAB29187.1	F (C-D) -1.58	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1)
55	AK014697 BAB29508.1	U (HI-D) 2.01	DC-specific transmembrane protein
	AK017185 BAB30625.1	U (C-D) 2.9	Ras-related protein Rab-30
	AK018132 BAB31086.1	U (C-D) 2.44	KIAA1001 protein

	AK018226 XP_110043.1	F (C-HI) -2.53	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin)
		F (C-D) -2.4	Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
5			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)
10	AK018485 BAB31233.1	F (C-HI) -2.46	similar to data source:SPTR, source key:Q60928, evidence:ISS~putative~similar to GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE) (GGT)
			Alternate: hypothetical protein FLJ90165
	C76314 NP_690023.1	U (C-D) 2.97	KIAA0432
15			Alternate: CDC5-like; CDC5 (cell division cycle 5, S. pombe, homolog)-like; Cell division cycle 5, S. pombe, homolog-like; Cdc5-related protein
	J03953 AAA37748.1	F (C-HI) -3.03	Chain A, ligand-free Glutathione S-Transferase
			Subclass: Chain A, ligand-free, Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
20			Subclass: Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase Mu 4
			Subclass: Chain A, glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2
			Subclass: Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)
			Subclass: Similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)
25	M12571 AAA57234.1	U (C-HI) 3.58	heat shock 70kDa protein
			Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
			Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
			Subclass: heat shock 70kD protein 1-like
30			Subclass: heat shock 70kDa protein 6 (HSP70B')
			Subclass: heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2
	M12573 AAA37863.1	U (C-D) 2.94	heat shock 70kDa protein

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		Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
		Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
		Subclass: heat shock 70kD protein 1-like
		Subclass: heat shock 70kDa protein 6 (HSP70B')
		Subclass: heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2
M62766 AAA37819.1	U (C-HI) 2.02	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
		Subclass: Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
M63245 AAA91867.1	U (C-HI) 3.05	aminolevulinate synthase
		Subclass: aminolevulinate synthase 1
		Subclass: 5-aminolevulinic acid synthase
		Subclass: 5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-E)
		Subclass: aminolevulinate, delta-, synthase 2; Aminolevulinate, delta-, synthase-2
		Subclass: Similar to aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)
NM_007395 NP_031421.1	F (C-IR) -2.16	activin A type IB receptor
		Subclass: activin A type IB receptor precursor; serine(threonine) protein kinase
		Subclass: activin A type IB receptor, isoform b precursor; serine(threonine) protein kinase
		Subclass: activin type I receptor SKR2, splice form 2
		Subclass: activin A type IB receptor, isoform c precursor; serine(threonine) protein kinase
		Subclass: activin type I receptor SKR2 splice form 3
		Subclass: transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa); transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kD)
NM_007437 NP_031463.1	U (C-IR) 3.02	aldehyde dehydrogenase 3A2; aldehyde dehydrogenase 10; aldehyde dehydrogenase 3 family, member A2; fatty aldehyde dehydrogenase
NM_007468 NP_031494.1	U (C-IR) 2.98	Apolipoprotein A-IV (Apo-AIV)
	U (C-D) 2.42	
	U (IR-D) 2.16	
NM_007472 NP_031498.1	F (C-IR) -2.17	aquaporin 1 (channel-forming integral protein, 28kD)
	U (IR-D) 2.38	

	NM_007474 NP_031500.1	F (C-IR) -2.07	aquaporin 8
5	NM_007494 NP_031520.1	F (C-D) -2.36	argininosuccinate synthetase
	NM_007585 NP_031611.1	U (C-IR) 3.49	annexin A2; annexin II; lipocortin II; Annexin II (lipocortin I); calpactin I, heavy polypeptide (p36); annexin II (lipocortin II; calpactin I, heavy polypeptide); annexin II (lipocortin II)
10		U (C-D) 4.83	
	NM_007630 NP_031656.1	F (IR-D) -5.28	cyclin B2
15	NM_007643 NP_031669.1	F (C-IR) -3.03	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I)
		U (C-D) 2.05	
		U (IR-D) 3.33	
20	NM_007659 NP_031685.1	U (C-IR) 3	cell division cycle 2 protein, isoform 1; cell division control protein 2 homolog; cyclin-dependent kinase 1; p34 protein kinase; cell cycle controller CDC2
		F (IR-D) -2.87	Alternate: Cyclin-Dependent Protein Kinase 2; Chain: A; Synonym: Cdk2; Ec: 2.7.1.37
	NM_007679 NP_031705.1	U (C-IR) 2.11	CCAAT/enhancer binding protein (C/EBP), delta
25	NM_007706 NP_031732.1	F (C-D) -2.51	suppressor of cytokine signaling-2; STAT induced STAT inhibitor-2; cytokine-inducible SH2 protein 2
30	NM_007760 NP_031786.1	U (C-IR) 2.57	carnitine acetyltransferase
		U (C-D) 2.16	Subclass: Carnitine O-acetyltransferase (Carnitine acetylase) (CAT) Subclass: carnitine acetyltransferase precursor, isoform 1 Subclass: carnitine acetyltransferase isoform 2
35	NM_007809 NP_031835.1	U (C-IR) 3.41	cytochrome P450, subfamily XVII polypeptide; steroid 17-alpha-monooxygenase; steroid 17-alpha-hydroxylase/17,20 lyase; cytochrome p450 XVIIA1
		U (C-D) 3.69	
40	NM_007811 NP_031837.1	F (C-IR) -17.03	Cytochrome P450 26 (Retinoic acid-metabolizing cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase)
		F (C-D) -3.81	
45	NM_007815 NP_031841.1	F (C-IR) -2.11	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase).
		F (C-D) -2.78	Subclass: Cytochrome P450 2C18 (CYPIIC18) (P450-6B/29C)

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		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17
		Subclass: cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
NM_007818 NP_031844.1	F (C-IR) -4.29	cytochrome P450, subfamily IIIA
	F (C-D) -8.15	Subclass: Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP3A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 5; nifedipine oxidase; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 7; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450 polypeptide 43 isoform 2; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 1; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 3; cytochrome P450 polypeptide 43
NM_007822 NP_031848.1	U (C-IR) 24.5	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase (CYP4A11)
	F (C-D) -5.06	
	F (IR-D) -7.06	
NM_007824 NP_031850.1	F (C-IR) -2.14	Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase)
	F (C-D) -3.09	
NM_007825 NP_031851.1	F (C-IR) -6.41 U (IR-D) 5.83	cytochrome P450, subfamily VIIB, polypeptide 1; oxysterol 7alpha-hydroxylase
NM_007837 NP_031863.1	U (C-IR) 2.98	DNA-damage-inducible transcript 3; C/EBP homologous protein; growth arrest- and DNA damage-inducible

	U (C-D) 2.16	
5	NM_007860 NP_031886.1	U (C-IR) 2.84 Type I iodothyronine deiodinase (Type-I 5'deiodinase) (DIOI) (Type 1 DI) (5DI)
	U (C-D) 2.06	
	NM_007870 NP_031896.1	F (C-IR) -2.2 deoxyribonuclease I-like 3
10	U (IR-D) 2.24	
	NM_007912 NP_031938.1	F (C-IR) -2.09 Epidermal growth factor receptor (Egfr)
	F (C-D) -2.69	
15	NM_007913 NP_031939.1	F (IR-D) -2.66 early growth response 1; G0S30
	NM_007980 NP_032006.1	U (C-IR) 3.49 intestinal fatty acid binding protein 2; Fatty acid-binding protein, intestinal; I-FABP; fatty acid binding protein 2, intestinal
20	U (C-D) 2.22	
	NM_008061 NP_032087.1	F (C-IR) -2.28 glucose-6-phosphatase, catalytic
	F (C-D) -2.14	
25	NM_008137 NP_032163.1	U (C-D) 3.01 guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14
	NM_008182 NP_032208.1	F (C-IR) -9.17 glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-aralkyltransferase A2; GST-gamma; HA subunit 2
30	F (C-D) -5.68	
	NM_008183 NP_032209.1	F (C-D) -2.27 glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-aralkyltransferase M2
35	NM_008184 NP_032210.1	F (C-D) -1.78 glutathione transferase
		Subclass: Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-aralkyltransferase M2



		Subclass: glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4
		Subclass: glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5
		Subclass: glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human
5	NM_008239 NP_032265.2	U (C-D) 2.23 winged helix/forkhead transcription factor
		U (IR-D) 2.15 Alternate: HNF-3/forkhead-like protein 1
10	NM_008245 NP_032271.1	F (C-D) -2.62 hematopoietically expressed homeobox; proline-rich homeodomain-containing transcription factor (HEX)
		U (IR-D) 2.05
15	NM_008295 NP_032321.1	F (C-IR) -2.43 hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1; Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid
		F (C-D) -5.64
		F (IR-D) -2.32
20	NM_008299 NP_032325.1	U (C-IR) 2.02 DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
		Alternate: similar to DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
25	NM_008303 NP_032329.1	F (C-D) -2.12 heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (chaperonin 10)
	NM_008322 NP_032348.1	F (C-D) -2.1 isocitrate dehydrogenase 2 (NADP+), mitochondrial; Isocitrate dehydrogenase, mitochondrial
30	NM_008341 NP_032367.1	F (C-IR) -3.37 insulin-like growth factor binding protein 1
		F (C-D) -3.47
		F (IR-D) -2.63
35	NM_008361 NP_032387.1	F (C-IR) -2.65 interleukin 1, beta
		F (C-D) -2.03
40	NM_008362 NP_032388.1	U (C-IR) 2.59 interleukin 1 receptor, type I
		F (IR-D) -2.22
	NM_008382 NP_032408.1	U (C-IR) 2.13 activin beta E
		Alternate: inhibin beta C chain preproprotein; activin beta-C chain
	NM_008495 NP_032521.1	F (C-IR) -2.65 beta-galactosidase binding lectin precursor; Lectin, galactose-binding, soluble, 1; galectin

		U (C-D) 2.32	
	NM_008509 NP_032535.1	F (C-D) -2.05	lipoprotein lipase
5		F (IR-D) -2.42	Subclass: lipoprotein lipase precursor
			Subclass: Similar to lipoprotein lipase
			Subclass: lipoprotein lipase
	NM_008587 NP_032613.1	F (C-IR) -2.1	c-mer proto-oncogene tyrosine kinase
10			
	NM_008597 NP_032623.1	U (IR-D) 2.36	matrix Gla protein (gamma-carboxyglutamate protein)
15	NM_008615 NP_032641.1	F (C-IR) -2.22	cytosolic malic enzyme 1; malic enzyme, cytoplasmic; malic enzyme 1, soluble; NADP-dependent malic enzyme; malate dehydrogenase; pyruvic-malic carboxylase
	NM_008742 NP_032768.1	F (C-IR) -2.68	neurotrophin 3
20	NM_008756 NP_032782.1	F (C-D) -2.04	occludin
	NM_008792 NP_032818.1	F (C-IR) -2.19	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5
25		F (C-D) -2.35	
	NM_008988 NP_033014.1	F (C-IR) -2.6	putative neuronal cell adhesion molecule (punc)
		F (C-D) -2.13	Subclass: putative neuronal cell adhesion molecule (punc)
30		U (IR-D) 4.12	Subclass: similar to punc
	NM_009127 NP_033153.1	F (C-IR) -2.15	Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)
		F (C-D) -3.29	
35		F (IR-D) -2.71	
	NM_009154 NP_033180.1	U (C-IR) 2.23	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, 5A
40	NM_009221 NP_033247.1	F (C-IR) -2.02	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor
	NM_009234 NP_033260.1	U (IR-D) 2.36	SRY (sex determining region Y)-box 11; SRY (sex-determining region Y)-box 11
45	NM_009252 NP_033278.1	U (C-D) 1.77	alpha1-antichymotrypsin

5	NM_009255 NP_033281.1	U (IR-D) 2.01	similar to tropomyosin, fibroblast - human
			Alternate: Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease inhibitor 7)
			Alternate: glia-derived neurite promoting factor precursor
	NM_009263 NP_033289.1	F (C-IR) -2.04	Osteopontin precursor (Bone sialoprotein 1) (Urinary stone protein) (Secreted phosphoprotein 1) (SPP-1) (Nephropontin) (Uropontin)
10	NM_009315 NP_033341.1	U (C-IR) 2.2	TBP-associated factor 6 Subclass:
			Subclass: TBP-associated factor 6 isoform gamma; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit
			Subclass: TBP-associated factor 6 isoform delta; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit
	NM_009344 NP_033370.1	U (IR-D) 2.1	pleckstrin homology-like domain, family A, member 1; PQ-rich protein
15			Alternate: Similar to T-cell death associated gene
	NM_009349 NP_033375.1	F (C-D) -2.04	Methyltransferase
			Subclass: Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)
			Subclass: indolethylamine N-methyltransferase; thioester S-methyltransferase-like
			Subclass: thioether S-methyltransferase-like; similar to P40936 (PID:g731019)
20			Subclass: nicotinamide N-methyltransferase
	NM_009366 NP_033392.1	U (C-IR) 2.06	transforming growth factor beta-stimulated protein TSC-22
		U (C-D) 2.89	
		U (IR-D) 2.64	
25	NM_009396 NP_033422.1	F (C-D) -2.5	tumor necrosis factor, alpha-induced protein 2
	NM_009425 NP_033451.1	F (IR-D) -10.21	tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related apoptosis inducing ligand TRAIL
	NM_009466 NP_033492.1	F (C-IR) -2.32	UDP-glucose dehydrogenase (uridine diphosphoglucose dehydrogenase)
		F (C-D) -2	
30			
35	NM_009669 NP_033799.1	F (C-IR) -3.13	Alpha-Amylase
			Subclass: amylase, alpha 2A; pancreatic; Amylase, pancreatic, alpha-2A
			Subclass: amylase, alpha 2B; pancreatic; Amylase, pancreatic, alpha-2B

		Subclass: similar to Alpha-amylase, salivary precursor (1,4-alpha-D-glucan glucanohydrolase)
		Subclass: amylase, alpha 1A; salivary; Amylase, salivary, alpha-1A
5	NM_009676 NP_033806.1	F (C-IR) -2.08 aldehyde oxidase 1
	NM_009689 NP_033819.1	U (C-IR) 3.67 baculoviral IAP repeat-containing protein 5; apoptosis inhibitor 4; survivin
10		F (IR-D) -3.5
	NM_009744 NP_033874.1	F (C-D) -4.15 B-cell lymphoma 6 (BCL6) protein; B-cell CLL/lymphoma-6; cys-his2 zinc finger transcription factor BCL5; zinc finger protein 51; lymphoma-associated zinc finger gene on chromosome 3
		U (IR-D) 2.11
15	NM_009748 NP_033878.1	F (C-IR) -2.03 Golgi vesicular membrane trafficking protein p18; Bet1 (S. cerevisiae) homolog; Bet1p homolog
		F (C-D) -2.15
	NM_009864 NP_033994.1	F (C-IR) -2.05 cadherin 1, type 1 preproprotein; calcium-dependent adhesion protein, epithelial; cadherin 1, E-cadherin (epithelial); uvomorulin; cell-CAM 120/80; Arc-1
20		
	NM_009895 NP_034025.1	U (IR-D) 2.45 cytokine-inducible SH2-containing protein
		Subclass: cytokine-inducible SH2-containing protein isoform 2; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling
		Subclass: cytokine-inducible SH2-containing protein isoform 1
25	NM_009964 NP_034094.1	U (IR-D) 2.06 crystallin, alpha B; crystallin, alpha-2; Rosenthal fiber component; heat-shock 20 kD like-protein
	NM_009993 NP_034123.1	F (C-D) -3.27 cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2 (cytochrome P450-1A2); dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase
30		
	NM_009998 NP_034128.1	F (C-IR) -2.61 cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6
		F (C-D) -2.33
35	NM_010000 NP_034130.1	U (C-IR) 34.21 cytochrome P450
		U (C-D) 8.32 Subclass: cytochrome P450-2B6
		F (IR-D) -3.81 Subclass: Cytochrome P450 2A13 (CYP1A13)
		Subclass: cytochrome P450 2A6
40		Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
		Subclass: cytochrome P450 2A4
		Subclass: Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)
		Subclass: cytochrome P450 2C8

		Subclass: cytochrome P450 2F1
		Subclass: cytochrome P450 2C18
		Subclass: cytochrome P450 2C9
		Subclass: cytochrome P450 2C10
5		Subclass: cytochrome P450 2C19
	NM_010001 NP_034131.1	F (C-IR) -2.43 cytochrome P450
		F (C-D) -2.56 Subclass: Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)
10		Subclass: cytochrome P450 2C19
		Subclass: cytochrome P450 2C9
		Subclass: cytochrome P450 2C10
		Subclass: cytochrome P450 2C8
15	NM_010012 NP_034142.1	F (C-IR) -2.08 cytochrome P450, subfamily VIIIB, polypeptide 1 (CYP8B1); 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-hydroxylase
	NM_010016 NP_034146.1	F (C-IR) -2.04 decay accelerating factor 1
20		U (IR-D) 2.14 Subclass: decay accelerating factor 1 for complement (CD55, Cromer blood group system); Decay-accelerating factor of complement
		Subclass: decay-acceleration factor 1 (Daf1)
	NM_010024 NP_034154.1	F (C-IR) -2.14 dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2); Dopachrome tautomerase (dopachrome delta-isomerase; tyrosinase-related protein 2)
25		F (C-D) -2.01
		U (IR-D) 2.28
	NM_010062 NP_034192.1	F (C-IR) -2 deoxyribonuclease
30		F (C-D) -2.4 Subclass: deoxyribonuclease II, lysosomal; DNase II, lysosomal
		Subclass: deoxyribonuclease II beta, isoform 1 precursor; DNase II-like acid DNase; endonuclease DLAD
	NM_010107 NP_034237.1	F (C-D) -2.18 ephrin-A1
35		
	NM_010121 NP_034251.1	U (C-IR) 2.15 eukaryotic translation initiation factor 2-alpha kinase 3; eukaryotic translation initiation factor 2 alpha kinase 3
		F (IR-D) -2.19
40	NM_010145 NP_034275.1	F (C-IR) -2.09 epoxide hydrolase 1, microsomal (xenobiotic); Epoxide hydroxylase 1, microsomal (xenobiotic)
		F (C-D) -2.09
	NM_010166 NP_034296.1	F (C-IR) -2.57 Eyes absent homolog 3 (EYA3)
45		

	NM_010187 NP_034317.1	F (C-IR) -2.18	Low affinity immunoglobulin gamma FC region receptor II-B precursor (FC-gamma RII-B) (FCRII-B) (IGG FC receptor II-B) (FC-gamma-RIIB) (CD32) (CDW32)
		U (IR-D) 2.55	
5	NM_010220 NP_034350.1	U (C-D) 2.02	FK506-binding protein 5; 51 kDa FK506-binding protein 5; 54 kDa progesterone receptor-associated immunophilin; T-cell FK506-binding protein; peptidylprolyl cis-trans isomerase; rotamase; FF1 antigen; HSP90-binding immunophilin
10	NM_010286 NP_034416.1	U (C-IR) 2.83	Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R)
		F (IR-D) -2.17	
15	NM_010324 NP_034454.1	F (C-D) -2.01	aspartate aminotransferase 1; glutamic-oxaloacetic transaminase 1, soluble
	NM_010354 NP_034484.1	U (C-IR) 2.03	gelsolin (amyloidosis, Finnish type); Gelsolin
20	NM_010357 NP_034487.1	F (C-IR) -2.17	glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-aryltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4
		F (C-D) -2.93	
25	NM_010361 NP_034491.1	F (C-IR) -2.46	glutathione S-transferase theta 2
		F (C-D) -2.25	
30	NM_010379 NP_034509.1	F (C-IR) -2.87	MHC class II histocompatibility antigen
		U (IR-D) 2.37	Subclass: MHC class II histocompatibility antigen DQw1-beta chain precursor
			Subclass: MHC class II HLA-DQ-beta-1
			Subclass: HLA class II histocompatibility antigen, DQ(W3) beta chain precursor
			Subclass: MHC class II histocompatibility antigen HLA-DQ beta chain (DQ4) precursor - human
35	NM_010401 NP_034531.1	F (C-IR) -2.39	histidine ammonia-lyase; Histidine ammonia-lyase (histidase)
		F (C-D) -2.21	
40	NM_010516 NP_034646.1	U (C-IR) 2.04	CYR61 protein
	NM_010544 NP_034674.1	U (C-IR) 2.45	Indian hedgehog protein (IHH) (HHG-2)
		F (IR-D) -2.47	

	NM_010565 NP_034695.1	U (C-IR) 2.28 inhibin beta C chain; activin beta-C chain
5	NM_010634 NP_034764.1	U (C-IR) 3.17 fatty acid binding protein 5 (psoriasis-associated); E-FABP
		F (IR-D) -5.62
	NM_010721 NP_034851.1	U (C-D) 7.08 lamin B1
10		
	NM_010877 NP_035007.1	U (C-HI) 2.02 Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH oxidase factor 2) (67 kDa neutrophil oxidase factor) (p67-phox)
15	NM_010924 NP_035054.1	F (C-HI) -2.45 nicotinamide N-methyltransferase
		F (C-D) -2.19
	NM_011058 NP_035188.1	U (C-HI) 2.3 platelet-derived growth factor receptor alpha polypeptide
20		
	NM_011125 NP_035255.1	F (C-HI) -2.01 phospholipid transfer protein
25	NM_011128 NP_035258.1	U (C-D) 2.35 pancreatic lipase-related protein 2
		U (HI-D) 2.73
	NM_011146 NP_035276.1	F (C-HI) -2.17 peroxisome proliferative activated receptor gamma, isoform 2; PPAR-gamma; peroxisome proliferator activated receptor gamma
30		
	NM_011169 NP_035299.1	F (HI-D) -2.08 prolactin receptor
35	NM_011172 NP_035302.1	F (C-D) -2 proline dehydrogenase; PRODH
	NM_011300 NP_035430.1	F (C-D) -2.11 ribosomal protein S7; 40S ribosomal protein S7
40	NM_011318 NP_035448.1	U (C-HI) 2.03 Serum Amyloid P Component (Sap)
		F (HI-D) -2.37
45	NM_011361 NP_035491.1	U (C-HI) 2.2 serine/threonine protein kinase sgk (serum/glucocorticoid regulated kinase)
	NM_011375 NP_035505.1	U (C-HI) 2.65 sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase); ganglioside G(M3) Synthase
		U (C-D) 2.16
50		

5	NM_011579 NP_035709.1	U (C-HI) 2.13	hypothetical protein R30953_1
	NM_011596 NP_035726.1	F (C-HI) -2.51	TJ6 protein
		F (C-D) -2.34	Alternate: ATPase, H+ transporter
		U (HI-D) 4.16	Subclass: ATPase, H+ transporting, lysosomal, non-catalytic accessory protein 1A, 110/116 kDa subunit; ATPase, H+ transporting, lysosomal non-catalytic accessory protein 1 (110/116kD); vacuolar proton pump, subunit 1; clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit; vacuolar proton translocating ATPase 116 kDa subunit A isoform 1; vacuolar adenosine triphosphatase subunit Ac116; H(+)-transporting two-sector ATPase, 116 kDa accessory protein A1; vacuolar-type H(+)-ATPase 115 kDa subunit
			Subclass: ATPase, H+ transporting, lysosomal V0 subunit a isoform 4; vacuolar proton pump 116 kDa accessory subunit; vacuolar proton pump, subunit 2; H(+)-transporting two-sector ATPase, noncatalytic accessory protein 1B; ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B; renal tubular acidosis; ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 2 (38kD)
10			Subclass: T-cell, immune regulator 1, isoform a; ATPase, H+ transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis
	NM_011676 NP_035806.1	U (C-D) 2.04	unc119 (C.elegans) homolog. Subclass: isoform a; unc119 (C.elegans) homolog; retinal protein 4
			Subclass: unc119 (C.elegans) homolog, isoform b; unc119 (C.elegans) homolog; retinal protein 4
15	NM_011693 NP_035823.1	U (C-D) 2.08	vascular cell adhesion molecule 1, isoform a ; CD106 antigen
	NM_011704 NP_035834.1	U (C-HI) 4.37	Vanin 1 (VNN1)
20		U (C-D) 3.14	
		U (HI-D) 2.37	
25	NM_011802 NP_035932.1	F (C-D) -2.08	ClpX caseinolytic protease X homolog; energy-dependent regulator of proteolysis; ClpX (caseinolytic protease X, E. coli)
	NM_011817 NP_035947.1	F (C-HI) -2.13	growth arrest and DNA damage inducible protein gamma (GADD45-gamma)
30	NM_011819 NP_035949.1	U (C-HI) 2.39	Growth/differentiation factor 15 (GDF-15); (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)
		U (C-D) 2	
		F (HI-D) -2.52	



	NM_011834 NP_035964.1	F (C-HI) -2.03	L-kynurenine/alpha-aminoadipate aminotransferase; kynurenine aminotransferase II
5	NM_011844 NP_035974.1	U (C-HI) 2.19	monoglyceride lipase
	NM_011850 NP_035980.1	F (HI-D) -2.03	short heterodimer partner; orphan nuclear receptor SHP; small heterodimer partner; nuclear receptor subfamily 0, group B, member 2
10	NM_011921 NP_036051.1	F (C-HI) -2.08	aldehyde dehydrogenase 1
			Subclass: aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
			Subclass: aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2
15			Subclass: aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6
			Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5
	NM_011994 NP_036124.1	U (C-HI) 2.27	ATP-binding cassette, sub-family D, member 2; adrenoleukodystrophy-like 1; hALDR
20	NM_012006 NP_036136.1	F (C-D) -2.24	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) Alternate: peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein Alternate: Similar to peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein
25	NM_013459 NP_038487.1	F (C-HI) -2.94	Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)
	NM_013490 NP_038518.1	F (HI-D) -2.04	choline kinase
30	NM_013541 NP_038569.1	F (C-D) -2.05	glutathione S-transferase
			Subclass: glutathione transferase pi
			Subclass: glutathione S-transferase-P1c
35			Subclass: Chain A, Glutathione S-Transferase P1-1
			Subclass: glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester synthase III
	NM_013565 NP_038593.1	U (HI-D) 2.05	Integrin alpha-3 (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c)
40	NM_013584 NP_038612.1	F (C-HI) -2.31	leukemia inhibitory factor receptor, LIF receptor [human, placenta, Peptide, 1078 aa]
		F (C-D) -2.46	

5	NM_013594 NP_038622.1	U (C-HI) 2.01	methyl-CpG binding domain protein 1
		U (C-D) 2.15	
10	NM_013646 NP_038674.1	F (HI-D) -2.02	RAR-related orphan receptor A,
			Subclass: RAR-related orphan receptor A, isoform a; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
			Subclass: RAR-related orphan receptor A, isoform c; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
			Subclass: RAR-related orphan receptor A, isoform b; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
			Subclass: RAR-related orphan receptor A, isoform d; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
15	NM_013692 NP_038720.1	U (C-D) 2.01	TGFB inducible early growth response
20	NM_013743 NP_038771.1	F (C-HI) -2.19	pyruvate dehydrogenase kinase, isoenzyme 4
	NM_013760 NP_038788.1	U (C-HI) 2.34	DnaJ (Hsp40) homolog, subfamily B, member 9; microvascular endothelial differentiation gene 1; DKFZP564F1862 protein; endoplasmic reticulum DnaJ homolog 4
25		U (C-D) 2.1	
	NM_013805 NP_038833.1	U (HI-D) 2.04	transmembrane protein claudin 5; androgen withdrawal and apoptosis induced protein RVP1 (rat)-like; Claudin-5 (transmembrane protein deleted in velocardiofacial syndrome)
	NM_013809 NP_038837.1	F (C-D) -2	cytochrome P450
			Subclass: Cytochrome P450 2A13 (CYP11A13)
30			Subclass: coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 -
			Subclass: Cytochrome P450 2A7 (CYP11A7) (P450-IIA4)
			Subclass: cytochrome P450 2A4 - human
			Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
			Subclass: cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily IIF, polypeptide 1 (H. sapiens)
			Subclass: cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6

		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYPIIC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYPIIC8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
5		Subclass: cytochrome P450, subfamily IIE, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)
		Subclass: cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P540, subfamily IIS, polypeptide 1
		Subclass: cytochrome P450, subfamily IIJ (arachidonic acid epoxigenase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase; Cytochrome P450, subfamily IIJ (arachidonic acid epoxigenase),
		Subclass: cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
10		Subclass: Cytochrome P450 2C17
		Subclass: Cytochrome P450 2C18 (CYPIIC18) (P450-6B/29C)
	NM_013888 NP_038916.1	F (HI-D) -2.04 J domain containing protein 1
15	NM_015763 NP_056578.1	F (C-HI) -3.7 Lipin 1
		U (C-D) 3.14
	NM_016696 NP_057905.1	U (C-D) 2.02 glypican 1
20		
	NM_016704 NP_057913.1	F (C-HI) -2.26 Complement component 6
		U (HI-D) 3.29
25	NM_016810 NP_058090.1	F (C-HI) -2.86 golgi SNAP receptor complex member 1; Golgi SNARE 28 kDa
	NM_016847 NP_058543.1	U (C-HI) 2.02 arginine vasopressin receptor 1A; V1a vasopressin receptor; vascular/hepatic-type arginine vasopressin receptor; antidiuretic hormone receptor 1A
30		F (HI-D) -2.03
	NM_016875 NP_058571.1	U (HI-D) 2.73 germ cell specific Y-box binding protein; contrin

	NM_016970 NP_058666.1	U (HI-D) 2.13	killer cell lectin-like receptor subfamily G, member 1; mast cell function-associated antigen (ITIM-containing)
5	NM_016974 NP_058670.1	U (C-HI) 2.79	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)
		U (C-D) 4.24	
		U (HI-D) 2.47	
10	NM_016978 NP_058674.1	F (C-D) -2.01	Ornithine aminotransferase
	NM_017480 NP_059508.1	U (C-HI) 6.6	inducible T-cell co-stimulator; activation-inducible lymphocyte immunomediatory molecule; inducible costimulator
15			
	NM_018776 NP_061246.1	F (C-HI) -2.07	cytokine receptor-like factor 3
		F (C-D) -2.11	
20	NM_018779 NP_061249.1	F (C-HI) -2.35	phosphodiesterase 3A, cGMP-inhibited
		F (C-D) -2.43	
25	NM_018791 NP_061261.1	U (C-HI) 2.32	Zinc finger protein
			Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)
			Subclass: zinc finger protein 226; Kruppel-associated box protein
			Subclass: Zinc finger protein ZNF45
30			Subclass: similar to Zinc finger protein 229
			Subclass: zinc finger protein 224
			Subclass: zinc finger protein 228
			Subclass: similar to ZNF228 protein
			Subclass: Zinc finger protein 234 (Zinc finger protein HZF4)
35			Subclass: similar to Zinc finger protein 234 (Zinc finger protein HZF4)
			Subclass: zinc finger protein 225
	NM_018817 NP_061287.1	U (C-HI) 2.27	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1
40	NM_018830 NP_061300.1	U (HI-D) 2.42	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2; N-acylsphingosine amidohydrolase 2; mitochondrial ceramidase; N-acylsphingosine amidohydrolase (acid ceramidase) 2
	NM_018861 NP_061349.1	U (C-HI) 2.18	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; Solute carrier family 1 (glutamate/neutral amino acid transporter),
45	NM_019415 NP_062288.1	U (C-HI) 2.06	Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter) (Na-Cl symporter)

	NM_019423 NP_062296.1	U (C-HI) 2.53	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
		U (C-D) 2.08	
5	NM_019499 NP_062372.1	F (HI-D) -2.04	MAD2-like 1; MAD2 (mitotic arrest deficient, yeast, homolog)-like 1; mitotic arrest deficient, yeast, homolog-like 1
10	NM_019521 NP_062394.1	U (C-D) 2.14	growth arrest-specific 6; AXL stimulatory factor
	NM_019545 NP_062418.1	U (C-HI) 2.31	hydroxyacid oxidase 3; medium-chain 2-hydroxy acid oxidase HAOX3; (S)-2-hydroxy-acid oxidase; glycolate oxidase
15	NM_019634 NP_062608.1	U (HI-D) 2.86	transmembrane 4 superfamily member 2; membrane component, x chromosome, surface marker 1; T-cell acute lymphoblastic leukemia associated antigen 1; transmembrane protein A15; tetraspanin protein; cell surface glycoprotein A15; CD231 antigen; transmembrane 4 superfamily 2b
	NM_019641 NP_062615.1	U (C-HI) 2.29	stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; stathmin; leukemia-associated phosphoprotein p18
		F (HI-D) -2.08	
20	NM_019643 NP_062617.1	U (C-HI) 2.02	TERA protein
	NM_019682 NP_062656.1	U (C-HI) 2.24	dynein, cytoplasmic, light polypeptide; Dynein, cytoplasmic, light chain (protein inhibitor of neuronal NOS); protein inhibitor of neuronal nitric oxide synthase
25	NM_019699 NP_062673.1	U (C-HI) 2.46	fatty acid desaturase 2; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2
	NM_019810 NP_062784.1	U (C-D) 2	solute carrier family 5 (sodium/glucose cotransporter), member 1; Human Na <sup>+</sup> /glucose cotransporter 1 mRNA, complete cds; solute carrier family 5 (sodium/glucose transporter), member 1
30	NM_019811 NP_062785.1	F (C-HI) -2.03	acetyl-CoA synthetase
		F (C-D) -2.11	Subclass: acetyl-CoA synthetase isoform a; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
			Subclass: acetyl-CoA synthetase isoform b; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
35	NM_019922 NP_064306.1	U (C-D) 2.05	cartilage associated protein
	NM_019977 NP_064361.1	U (C-HI) 2.51	unknown protein
40			Alternate: aldehyde reductase (aldose reductase) like 6; similar to mouse aldehyde reductase 6 (renal); myo-inositol oxygenase; kidney-specific protein 32

		Alternate: kidney-specific protein 32
	NM_019992 NP_064376.1	U (C-HI) 2.06 BCR downstream signaling 1
		U (C-D) 2.23
5		U (HI-D) 2.12
	NM_020013 NP_064397.1	U (C-HI) 6 fibroblast growth factor 21
		U (C-D) 5.03
		F (HI-D) -3.06
10	NM_020277 NP_064673.1	U (C-D) 2.05 transient receptor potential cation channel, subfamily M, member 5; MLSN1 and TRP-related; MLSN1- and TRP-related; LTRPC5 protein
		U (HI-D) 2.32
15	NM_020564 NP_065589.1	F (C-HI) -2.84 sulfotransferase family, cytosolic, 2B, member 1; sulfotransferase family 2B, member 1
		F (C-D) -2.36 Subclass: hydroxysteroid sulfotransferase SULT2B1a
		U (HI-D) 2.6 Subclass: hydroxysteroid sulfotransferase SULT2B1b
20	NM_020570 NP_065595.1	U (C-HI) 2.55 X-ray repair cross complementing protein 2; X-ray repair, complementing defective, repair in Chinese hamster; DNA repair protein XRCC2
	NM_021307 NP_067282.1	F (C-HI) -2.44 Zinc finger protein
		Subclass: zinc finger protein 228
25		Subclass: similar to ZNF228 protein
		Subclass: Zinc finger protein 226
		Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)
		Subclass: Hypothetical zinc finger-like protein
		Subclass: similar to Zinc finger protein 229
30		Subclass: Zinc finger protein ZNF45
	NM_021366 NP_067341.1	U (C-HI) 2 Kruppel-like factor 13; transcription factor NSLP1; novel Sp1 like zinc finger transcription factor; RANTES factor of late activated T lymphocytes-1; basic transcription element binding protein 3
35	NM_022331 NP_071726.1	U (C-HI) 3 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene
		U (C-D) 2.29
	NM_023154 NP_075643.1	F (C-HI) -2.39 Similar to RIKEN cDNA 0610025L15 gene product
40		F (C-D) -2.48
	NM_023184 NP_075673.1	U (C-HI) 2.34 Kruppel-like factor 15; KKLf protein; kidney-enriched Kruppel-like factor
45	NM_023341 NP_075830.1	F (C-HI) -2.05 chaperone
		Subclass: chaperone-ABC1-like
		Subclass: chaperone, ABC1 activity of bc1 complex like

		Alternate: unnamed protein product
5	NM_023455 NP_075944.1	F (C-HI) -2.39 putative N-acetyltransferase Camello 2
		F (C-D) -2.04 Alternate: N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
		Alternate: GLA
		Alternate: kidney- and liver-specific gene product
		Alternate: hypothetical protein TSC501
10	NM_023719 NP_076208.1	U (C-HI) 2.36 thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3
		U (C-D) 2.42
15	NM_023737 NP_076226.1	F (C-HI) -2.07 enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
	NM_023740 NP_076229.1	F (C-HI) -1.7 PP3774
		F (C-D) -2.35 Alternate: Similar to RIKEN cDNA 1500015N03 gene product
20		U (HI-D) 2.52
	NM_023850 NP_076339.1	F (C-D) -2.03 carbohydrate (keratan sulfate Gal-6) sulfotransferase 1; carbohydrate (chondroitin 6/keratan) sulfotransferase 1
25	NM_025404 NP_079680.1	F (C-HI) -2.24 ADP-ribosylation factor
		F (C-D) -2.03 Subclass: ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6
		Subclass: similar to ADP-ribosylation-like 4
		Subclass: ADP-ribosylation factor-like 7
30		Subclass: ADP ribosylation factor-like protein
	NM_025429 NP_079705.1	F (C-HI) -3.51 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
		F (C-D) -3.01
35	NM_025566 NP_079842.1	U (C-HI) 2 hypothetical protein MGC17791
		U (C-D) 2.25 Alternate: similar to RIKEN cDNA 2600017J23 gene product
40	NM_025631 NP_079907.1	F (C-HI) -2.25 hypothetical protein dJ726C3.2
		F (C-D) -2.16
	NM_025754 NP_080030.1	F (C-D) -2.13 aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase
45	NM_026104 NP_080380.1	F (C-HI) -2.22 similar to RIKEN cDNA 1700095F04 gene product
		Alternate: unnamed protein product

5	NM_026156 NP_080432.1	U (C-D) 3.75	similar to PP3898
			Alternate: XAB2
			Alternate: KIAA1177 protein
			Alternate: HCNP protein; XPA-binding protein 2
			Alternate: Similar to HCNP protein; XPA-binding protein 2
10			Alternate: FLJ00081 protein
	NM_026228 NP_080504.1	U (C-D) 4.88	protein up-regulated by BCG-CWS
			Alternate: unnamed protein product
			Alternate: KIAA0062
			Alternate: similar to KIAA0062
15			Alternate: Unknown (protein for MGC:23235)
	NM_027000 NP_081276.1	F (C-HI) -2.13	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB)
			Alternate: G protein-binding protein CRFG; GTP-binding protein
			Alternate: G protein-binding protein CRFG
			Alternate: putative G-binding protein
20			Alternate: unnamed protein product
	NM_028089 NP_082365.1	F (C-HI) -4.31	cytochrome P-450
		F (C-D) -5.26	Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase
			Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
			Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
25			Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
			Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
			Subclass: cytochrome P450 2C17
30	NM_028780 NP_083056.1	U (C-D) 2	transmembrane 9 superfamily
			Subclass: transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1
			Subclass: transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2
			Subclass: similar to Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)
			Subclass: transmembrane protein TM9SF3
35			Alternate: SM-11044 binding protein
			Alternate: KIAA0255 gene product
			Alternate: endomembrane protein emp70 precursor isolog



		Alternate: unnamed protein product
		Alternate: unnamed protein product
5	NM_029813 NP_084089.1	F (C-D) -2.4 zinc finger protein
		Subclass: zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
		Subclass: similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
		Subclass: similar to zinc finger protein 91 (HPF7, HTF10)
10		Subclass: zinc finger protein 180 (HHZ168)
		Subclass: zinc finger protein 136 (clone pHZ-20)
		Subclass: KIAA1710 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1710
		Subclass: Zinc finger protein 93 (Zinc finger protein HTF34)
15		Subclass: zinc finger protein 135 (clone pHZ-17)
		Subclass: zinc finger protein 85 (HPF4, HTF1)
		Subclass: KIAA1198 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1198
		Subclass: similar to Zinc finger protein 135
20		Subclass: similar to Zinc finger protein 93 (Zinc finger protein HTF34)
		Subclass: zinc finger protein 91 (HPF7, HTF10)
		Subclass: zinc finger protein 84 (HPF2)
		Subclass: finger protein 2, placental
		similar to KRAB zinc finger protein KR18
25		Subclass: zinc finger protein AF020591
		Subclass: kruppel-related zinc finger protein
		Subclass: Similar to zinc finger protein 208
		Subclass: zinc finger protein 71; endothelial zinc finger protein induced by tumor necrosis factor alpha
		Subclass: zinc finger protein 37 homolog (mouse); Zinc finger protein-37, mouse, homolog of; zinc finger protein homologous to Zfp37 in mouse
30		Subclass: zinc finger protein 328
		Subclass: similar to zinc finger protein 29
		Subclass: zinc finger protein 268
		Similar to zinc finger protein 208
		Subclass: Zinc finger protein ZNF45
35		Subclass: zinc finger protein 16 (KOX 9)
		Subclass: similar to Zinc finger protein 85
		Subclass: zinc finger protein 43 (HTF6)
		Subclass: similar to Zinc finger protein 35 (Zfp-35)
		Subclass: zinc finger protein 228
40		Subclass: similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)
		Subclass: similar to Zinc finger protein 184
		Subclass: zinc finger protein 177
		Subclass: bB479F17.3 (zinc finger protein 41)
		Subclass: similar to Zinc finger protein 41
45		Subclass: zinc finger protein 287
		Subclass: zinc finger protein 331; zinc finger protein 463; C2H2-like zinc finger protein

		Subclass: zinc finger protein 271
		Subclass: Hypothetical zinc finger protein KIAA1473
		Subclass: similar to Hypothetical zinc finger protein KIAA1473
		Subclass: similar to Hypothetical zinc finger protein KIAA1956
5		Subclass: KRAB zinc finger protein
		Subclass: KIAA1956 protein
		Subclass: TRAF6-inhibitory zinc finger protein; TRAF6-binding zinc finger protein
		Alternate: hypothetical protein
		Subclass: FLJ40981
10		Subclass: similar to hypothetical protein FLJ40981
		Subclass: hypothetical protein FLJ21628
		Subclass: hypothetical protein FLJ32191
		Subclass: hypothetical protein DKFZp572C163.1
		Subclass: hypothetical protein FLJ30932
15		Subclass: hypothetical protein FLJ14345
		Subclass: hypothetical protein FLJ90396
		Subclass: hypothetical protein FLJ31526
		Subclass: hypothetical protein DKFZp572P0920.1
20	NM_030887 NP_112149.1	U (C-HI) 2.07 Jun dimerization protein
	NM_031162 NP_112439.1	U (C-HI) 2.49 CD3Z antigen, zeta polypeptide (TIT3 complex)
25	NM_032400 NP_115776.1	F (C-HI) -2.79 G protein-coupled receptor 91
		U (HI-D) 3.03
	NM_033146 NP_149158.1	F (C-D) -2.03 Protein CGI-112
30		Alternate: similar to Protein CGI-112
	NM_053200 NP_444430.1	F (C-HI) -2.04 carboxylesterase 3; brain carboxylesterase BR3
35	NM_053215 NP_444445.1	F (C-HI) -1.98 UDP glycosyltransferase; UDP-glucuronyltransferase
		F (C-D) -3.23 Subclass: UDP glycosyltransferase 2 family, polypeptide B17; UDP-glucuronyltransferase, family 2, beta-17
		Subclass: similar to UDP-glucuronosyltransferase 2B15 precursor, microsomal (UDPGT) (UDPGTH-3) (HLUG4)
		Subclass: UDP glycosyltransferase 2 family, polypeptide B15; UDP-glucuronyltransferase, family 2, beta-15
40		Subclass: UDP glycosyltransferase 2 family, polypeptide B4; UDP-glucuronyltransferase, family 2, beta-4
		Subclass: similar to UDP-glucuronosyltransferase 2B4 precursor, microsomal (UDPGT) (Hyodeoxycholic acid) (HLUG25) (UDPGTH-1)
		Subclass: UDP glycosyltransferase 2 family, polypeptide B7; UDP-glucuronyltransferase, family 2, beta-7

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		Subclass: UDP glycosyltransferase 2 family, polypeptide A1; UDP glucuronosyltransferase 2 family, polypeptide A1
		Subclass: UDP glycosyltransferase 2 family, polypeptide B11
		Subclass: UDP glycosyltransferase 2 family, polypeptide B10
		Subclass: UDP glycosyltransferase 2 family, polypeptide B28
S80191 AAB21335.1	F (C-D) -1.61	Unknown (protein for MGC:9220)
		Alternate: carboxylesterase
		Subclass: carboxylesterase 1(monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)
		Subclass: acyl coenzyme A:cholesterol acyltransferase
		Subclass: brain carboxylesterase hBr1
		Subclass: brain carboxylesterase hBr2
		Subclass: egasyn
		Subclass: Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)
		Subclass: carboxylesterase 3; brain carboxylesterase BR3
		Subclass: serine esterase N-terminal truncated (503 AA)
		Subclass: carboxylesterase 2; intestinal carboxylesterase; liver carboxylesterase-2
		Subclass: Similar to carboxylesterase 2 (intestine, liver)
U38940 AAA85125.1	F (C-HI) -3.11	asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein
	F (C-D) -2.11	
U67189 AAB50619.1	U (C-HI) 3.17	Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R) (A28-RGS14P)
U70139 AAB62717.1	U (C-D) 3.08	nocturnin
	U (HI-D) 2.08	
U70210 AAC53593.1	U (C-D) 2.06	Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)
		Alternate: similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)
X71479 CAA50585.1	F (C-HI) -3.57	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase
	F (C-D) -2.54	
	U (HI-D) 2.82	
X82786 CAA58026.1	U (C-HI) 4.07	antigen identified by monoclonal antibody Ki-67; Proliferation-related Ki-67 antigen
	F (HI-D) -4.25	

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NM_011369		
NP_035499.1	U:(C-IR)+2.13 F:(IR-D)-2.53	Shc SH2-domain binding protein
		Subclass: likely ortholog of mouse Shc SH2-domain binding protein 1
		(hypothetical protein FLJ22009)

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CLAIMS

1. A method of protecting a human subject from progression from a normoinsulinemic state to a  
5 hyperinsulinemic state, or from either to a type II diabetic state, which comprises administering to the subject a protective amount of an agent which is

10 (1) a polypeptide which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group  
15 consisting of human proteins within at least one of the human protein classes set forth in master table 2, subtables 2A and 2C,

or

20 (2) an expression vector encoding the polypeptide of (1) above and expressible in a human cell, under conditions conducive to expression of the polypeptide of (1);

25 where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state.

2. A method of protecting a human subject from progression from a normoinsulinemic state to a hyperinsulinemic state,  
30 or from either to a type II diabetic state which comprises administering to the subject a protective amount of an agent which is

35 (1) an antagonist of a polypeptide, occurring in said subject, which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtable 1B and



1C, or (b) selected from the group consisting of human proteins belonging to at least one of the human protein classes set forth in master table 2, subtables 2B and 2C,

- 5 (2) an anti-sense vector which inhibits expression of said polypeptide in said subject,

where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or  
10 from either to a type II diabetic state.

3. A method of screening for human subjects who are prone to progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic  
15 state, which comprises assaying tissue or body fluid samples from said subjects to determine the level of expression of a "favorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a  
20 reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group consisting of human proteins within at least one of the human protein classes set forth in master table 2, subtables  
25 2A and 2C,

and directly correlating the level of expression of said marker gene with the propensity to progression in said patient.

30

4. A method of screening for human subjects who have a propensity for progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises assaying tissue or body  
35 fluid samples from said subjects to determine the level of expression of an "unfavorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively

identical in sequence to a reference protein which is (a)  
selected from the group consisting of mouse and human  
proteins set forth in master table 1, subtable 1B and 1C, or  
(b) selected from the group consisting of human proteins  
5 belonging to at least one of the human protein classes set  
forth in master table 2, subtables 2B and 2C,

and inversely correlating the level of expression of said  
marker gene with the propensity to progression in said  
10 patient.

5. The method of claims 1 or 3 in which the reference  
protein is of subtable 1A or of a class set forth in  
subtable 2A.  
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6. The method of claims 1 or 3 in which the reference  
protein is of subtable 1B or of a class set forth in  
subtable 2B.

20 7. The method of any one of claims 1-6 in which (a) applies.

8. The method of any one of claims 1-7 in which the  
reference protein is a human protein.  
25

9. The method of any one of claims 1-7 in which the  
reference protein is a mouse protein.

10. The method of any one of claims 3 or 4 in which the  
level of expression of the marker protein is ascertained by  
measuring the level of the corresponding messenger RNA.  
30

11. The method of any one of claims 3 or 4 in which the  
level of expression is ascertained by measuring the level of  
a protein encoded by said marker gene.  
35

12. The method of any one of claims 1-9 in which said  
polypeptide is at least 80% identical or at least highly  
conservatively identical to said reference protein.

13. The method of any one of claims 1-10 in which said polypeptide is at least 90% identical to said reference protein.

5 14. The method of any one of claims 1-11 in which said polypeptide is identical to said reference protein.

10 15. The method of any one of claims 1-14 in which the E-value cited for the reference protein in Master Table 1 is not more than  $e^{-6}$ .

16. The method of claim 15 in which the E-value cited for the reference protein in Master Table 1 is less than  $e^{-10}$ .

15 17. The method of claim 17 in which the E value calculated by BLASTN or BLASTX would be less than  $e^{-15}$ , more preferably less than  $e^{-20}$ , still more preferably less than  $e^{-40}$ , even more preferably less than  $e^{-60}$ , considerably more preferably less than  $e^{-80}$ , and most preferably less than  $e^{-100}$ .

20 18. The method of any of claims 2-17 in which the antagonist is an antibody, or an antigen-specific binding fragment of an antibody.

25 19. The method of any of claims 2-17 in which the antagonist is a peptide, peptoid, nucleic acid, or peptide nucleic acid oligomer.

30 20. The method of any of claims 2-17 in which the antagonist is an organic molecule with a molecular weight of less than 500 daltons.

35 21. The method of claim 20 in which said organic molecule is identifiable as a molecule which binds said polypeptide by screening a combinatorial library.

**ABSTRACT OF THE DISCLOSURE**

5        Mouse genes differentially expressed in comparisons of  
normal vs. hyperinsulinemic, hyperinsulinemic vs. type 2  
diabetic, and normal vs. type 2 diabetic liver by gene chip  
analysis have been identified, as have corresponding human  
genes and proteins. The human molecules, or antagonists  
10 thereof, may be used for protection against hyperinsulinemia  
or type 2 diabetes, or their sequelae.

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